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OM protein - protein search, using sw model.

Run on: January 6, 2004, 16:04:46 ; search time 41 Seconds

(without alignments) 96.784 Million cell updates/sec

Title: US-09-774-940A-1
 Perfect score: 139
 Sequence: 1 YQCETCGKSPSDKSNLTHRLRIHTG 25

Scoring table: BIOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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22: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*

23: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2003.DAT:*

10: 106 76.3 448 22 AAM80249 Human protein SEQ
 11: 106 76.3 480 23 AAM88967 Human zinc finger
 12: 106 76.3 555 22 AAM79265 Human protein S80
 13: 105 76.3 555 22 AAB83576 Human protein seq
 14: 105 75.5 593 22 ABB10366 Drosophila melanogaster
 15: 104 74.8 362 23 ABG70216 Human prey protein
 16: 104 74.8 525 22 ABG47725 Human liver peptid
 17: 104 74.8 525 22 ABB27702 Human peptide #353
 18: 104 74.8 525 22 ABB32873 Human peptide #353
 19: 104 74.8 525 22 ABB18355 Protein #354 enco
 20: 104 74.8 525 22 AAM53675 Human brain expres
 21: 104 74.8 525 22 AAM66059 Human bone marrow
 22: 104 74.8 525 22 AAM13928 Human peptide #352
 23: 104 74.8 525 22 AAM26334 Human peptide #353
 24: 104 74.8 525 22 AAM01671 Human peptide #353
 25: 104 74.8 525 22 ABB50665 Human peptide enco
 26: 104 74.8 525 22 ABB57922 Human peptide enco
 27: 102 73.4 25 23 ABP07824 Novel human diaco
 28: 102 73.4 25 23 ABP05403 Zinc finger zinc fin
 29: 102 73.4 25 23 ABP05403 Zinc finger consen
 30: 102 73.4 25 23 ABP05403 Zinc finger consen
 31: 102 73.4 25 23 ABP05403 Zinc finger consen
 32: 102 73.4 25 24 ABP55217 Zinc finger zinc fin
 33: 102 73.4 25 24 ABP09200 Zinc finger DNA bi
 34: 102 73.4 25 23 ABG19380 Zinc finger consen
 35: 102 73.4 25 22 ABP05278 Zinc finger zinc fin
 36: 102 73.4 25 22 ABP05278 Zinc finger zinc fin
 37: 101 72.7 208 24 ABP41433 Zinc finger zinc fin
 38: 101 72.7 338 22 AAM3945 Zinc finger zinc fin
 39: 101 72.7 517 22 ABP03375 Zinc finger zinc fin
 40: 101 72.7 577 23 AAE14680 Novel human diagno
 41: 100 71.9 26 22 AAM71559 Human transcriptio
 42: 100 71.9 236 23 ABP0418 Consensus zinc fin
 43: 100 71.9 1050 22 ABP09685 Human ovarian anti
 44: 100 71.9 1212 22 ABP03999 Novel human diagno
 45: 100 71.9 1230 22 AAV30831 Novel human secret

ALIGNMENTS

RESULT 1
 AAY33363
 ID AAY3363 standard; peptide; 29 AA.
 XX
 AC AAY3363;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Consensus zinc finger peptide motif 2.
 XX
 KW Zinc finger; DNA binding; Cys2-His2 class; 5-methylcytosine; meC;
 KW diagnostic; detection; chimera.
 XX
 OS Unidentified.
 XX
 PN WO9447656-A2.
 XX
 PD 23-SRP-1999.
 XX
 PR 17-MAR-1999; 99W0-GB00816.
 PR 17-MAR-1998; 98GB-0005576.
 PR 31-MAR-1998; 98GB-0006895.
 PR 03-APR-1998; 98GB-0007246.
 PR (MEDI-) MEDICAL RES COUNCIL.
 PR Choo Y, Isalan M;
 PR DR WPI; 1999-562106/47.
 PR New zinc finger polypeptides that bind DNA containing modified bases,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	108	77.7	29	20 AAY33363	Consensus zinc fin
2	108	77.7	29	20 AAW78386	Synthetic Cys2-His
3	108	77.7	29	20 AAW84303	Consensus zinc fin
4	108	77.7	29	20 AAW87699	Consensus zinc fin
5	108	77.7	29	21 AAX94377	Zinc finger consen
6	108	77.7	29	22 AAU05197	Zinc finger protei
7	108	77.7	29	22 AAG63227	Amino acid sequenc
8	108	77.7	29	22 AAB20022	Zinc finger consen
9	106	76.3	24 ABB19775	Human MP21 protein	

PT used as diagnostic and research reagents and for regulating gene transcription -

Claim 20; Page 10; 56pp; English.

This invention describes a novel zinc finger (ZF) polypeptide (I) that binds to a target DNA sequence (II) containing a modified base but that is otherwise identical to an otherwise identical sequence containing the equivalent unmodified base. The invention also describes methods for preparing a DNA-binding polypeptide of the Cys2-His2 ZF class, able to recognize sequences containing a 5-methylcytosine (m₅C) residue. (I) are used as diagnostic reagents for detecting modified nucleic acids in complex mixture, including differentiation of single-base modifications, in research and to produce chimeras, e.g., by fusion to a catalytic domain of a restriction enzyme (the product can then cleave only modified DNA), or to a DNA cleavage or activating domain (to give products that can regulate gene transcription, by sequence-specific cleavage or activation, dependent on presence of a modified base). (I) recognize modified bases in preference to unmodified ones, in a sequence-dependent manner, so have extremely high specificity. This sequence represents a zinc finger consensus motif described in the method of the invention.

AA SQ Sequence 29 AA;

Query Match 77.7%; Score 108; DB 20; Length 29;

Matches	Best Local Similarity	Pred. Nc
19;	Conservative	2;

1 YOCEIICGKSFSDKSNJTRHLRIHTG 25

Db 2 YKCSECGKAFSQSNLTRHQRIHTG 26

RESULT 2

AAW78386
ID AAW78386 standard; peptide; 29 AA.

XX
AC
AAW78386;

XX
DT
11-MAY-1999 (first entry)

XX DE YY synthetic Cys2-His2 zinc finger protein

KW Zinc finger; target sequence; binding
KW Drosophila; mutation site; functional domain

synthetic.

XX
PN
WO98533060-A1:

XX
PD
26-NOV-1998.

XX
PF 26-MAY-1998; 98WO-GB01516.

XX
PR
23-MAY-1997; 97GB-0010809.

XX
PA
VV
(MEDI -) MEDICAL RES COUNCIL.

AA
PI
YY
Choo Y, Isalan M, Klug A;

DR
XX
WPI; 1999-045309/04.

PT PT
Rules for designing zinc finger nucleic acid sequences specific for any base quadruplet - review

PT specific amino acids in the alpha-helix
PT detect target nucleic acids, e.g. for

PT
XX phosphorylation sites

Claim 14; Page 41; 57pp; English.

This sequence represents a consensus zinc finger sequence for a model zinc finger of the Cys₂-His₂ zinc finger (ZF) class (AAW78382). The ZF are generated so that they are able to bind a nucleic acid quadruplet in a

Query Match Score 108; DB 22; Length 29;

```

Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
ID AAB0022 standard; Peptide; 29 AA
ID AAB0022

```

1 YOCBICGKSFSDKSNLTRHLRIHTG 25

RESULT 7
AAG63227
ID AAG63327 standard. nonradio. 20 20

OS Synthetic.
 XX
 PN WO200100815-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-MAY-2000; 2000WO-GB02080.
 XX
 PR 28-MAY-1999; 99GB-0012635.
 PR 24-JAN-2000; 2000GB-0001582.
 XX
 PA (END-) GENIAQ LTD.
 XX
 PI Choo Y, Ullman CGU;
 XX
 DR WPT; 2001-123005/13.
 XX
 The present sequence is that of a consensus zinc finger structure.
 The invention relates to molecular switches and methods for identifying and selecting such switches for use in modulating gene expression, comprising selecting complexes of two molecules and a ligand whose binding differs in the presence or absence of the ligand - Disclosure; Page 29; 125pp; English.
 The invention relates to a novel method for identifying a candidate p21 pathway modulating agent. The novel method comprises contacting an assay system, comprising a purified Me21 polypeptide (modifier of p21) or nucleic acid, with a test agent under conditions, so that but for the presence of a test agent, the assay system provides a reference activity and detection of test agent-biased activity of the assay system. The novel method of the invention is useful for identifying a candidate p21 pathway modulating agent. The invention also includes a method for modulating the p21 pathway of a cell, and a method for diagnosing a disease e.g. cancer in a patient. The identified modulators are useful in diagnosis, therapy and pharmaceutical development. The modulators are useful in a variety of diagnostic and therapeutic applications including angiogenic, apoptotic and cell proliferation disorders. This sequence represents an MP21 protein of the invention.
 XX
 Sequence 29 AA:
 Query Match 77.7%; Score 108; DB 22; Length 29;
 Best Local Similarity 76.0%; Pred. No. 1.1e-08;
 Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YQCEIGKGSFSQSKSNLTRHLRHTG 25
 2 YKCSECGKAFSKQSNLTRHQRIHTG 26
 Db
 RESULT 9
 ABJ19775
 ID ABJ19775 standard; Protein; 242 AA.
 XX
 AC ABJ19775;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Human MP21 protein Kox21 SEQ ID NO 55.
 XX
 KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic; cell proliferation disorder; MP21.
 XX
 OS Homo sapiens.
 XX
 WO2003006930-A1.
 XX
 PD 23-JAN-2003.
 XX
 PR 10-JUL-2002; 2002WO-US21549.
 XX
 PR 12-JUL-2001; 2001US-305017P.
 PR 10-OCT-2001; 2001US-328491P.
 PR 15-FEB-2002; 2002US-357452P.
 XX
 PA (END-) HYSSQ INC.
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
 XX
 DR N-FSDB; ABT17049.
 XX
 PT Identifying candidate p21 pathway modulator, by contacting an assay system having modifiers of p21 polypeptide or gene with a test agent to provide a reference activity in system and detecting test agent-biased activity -
 PT
 XX
 PS Examples; Page 176-177; 199pp; English.
 XX
 CC The invention relates to a novel method for identifying a candidate p21 pathway modulating agent. The novel method comprises contacting an assay system, comprising a purified Me21 polypeptide (modifier of p21) or nucleic acid, with a test agent under conditions, so that but for the presence of a test agent, the assay system provides a reference activity and detection of test agent-biased activity of the assay system. The novel method of the invention is useful for identifying a candidate p21 pathway modulating agent. The invention also includes a method for modulating the p21 pathway of a cell, and a method for diagnosing a disease e.g. cancer in a patient. The identified modulators are useful in diagnosis, therapy and pharmaceutical development. The modulators are useful in a variety of diagnostic and therapeutic applications including angiogenic, apoptotic and cell proliferation disorders. This sequence represents an MP21 protein of the invention.
 XX
 Sequence 242 AA:
 Query Match 76.3%; Score 106; DB 24; Length 242;
 Best Local Similarity 72.0%; Pred. No. 2.1e-07;
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YQCEIGKGSFSQSKSNLTRHLRHTG 25
 92 YECNECGKSPSEKSTLTKLRLRHTG 116
 Db
 RESULT 10
 AAM80249
 ID AAM80249 standard; Protein; 448 AA.
 XX
 AC AAM80249;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 395.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 WO200115190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PR 05-FEB-2001; 2001WO-US04038.
 XX
 PR 03-FEB-2000; 2000US-049694.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2001; 2001US-0620335.
 PR 01-SEP-2000; 2000US-065496.
 PR 15-SEP-2000; 2000US-066351.
 PR 20-OCT-2000; 2000US-069335.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (END-) HYSSQ INC.

CC activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK2581), 2111 (AAK5282) and 3666 (AAW0020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

SQ Sequence 555 AA;

Query Match 76.3%; Score 106; DB 22; Length 555;
 Best Local Similarity 68.0%; Pred. No. 5.3e-07; Indels 0; Gaps 0;
 Matches 17; Conservative 4; Mismatches 4; Sq

1 YQCEIIGKSFSDKSNITRHURHTG 25
 Db 244 YKCDILOGKVFSQKSNLARHHRVHTG 268

RESULT 13

AAB93575

ID AAB93575 standard; Protein; 555 AA.

XX

AC AAB93575;

XX

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:12988.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PR 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248035.

XX

PR 27-AUG-1999; 99JP-0300255.

XX

PR 11-JAN-2000; 2000EP-0118776.

XX

PR 03-MAY-2000; 2000EP-0183767.

XX

PR 09-JUN-2000; 2000EP-0241899.

XX

PA (HELI-) HELIX RES INST.

XX

PT Ota T, Isocai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX

PT Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -

XX

PS Claim 8; SEQ ID 12988; 2537pp + CD ROM; English.

XX

CC The present invention describes primer sets for synthesising 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC gene therapy. The primers are useful for synthesising polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAB03166 to AAB13628 and AAB11633 to AAB18742 represent human cDNA sequences; AAB22446 to AAB95893 represent human amino acid sequences; and AAB13629 to AAB13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

SQ Sequence 555 AA;

Query Match 76.3%; Score 106; DB 22; Length 555;
 Best Local Similarity 68.0%; Pred. No. 5.3e-07; Indels 0; Gaps 0;
 Matches 17; Conservative 4; Mismatches 4; Sq

1 YQCEIIGKSFSDKSNITRHURHTG 25
 Db 244 YKCDILOGKVFSQKSNLARHHRVHTG 268

RESULT 14

ABB70360

ID ABB70360 standard; Protein; 593 AA.

XX

AC ABB70360;

XX

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 37872.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PA (PEKE) PE CORP NY.

XX

PD 27-SEP-2001.

XX

PR 23-MAR-2001; 2001WO-US09231.

XX

PR 23-MAR-2000; 2000US-191637P.

XX

PR 11-JUL-2000; 2000US-064150.

XX

PA (PEKE) PE CORP NY.

XX

PT Venter JC, Adams M, Li PHD, Myers EW;

XX

DR WPI; 2001-656860/75.

XX

DR N-FSDB; ABL14463.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

XX

PS Disclosure; SEQ ID NO 37872; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention is

CC disclosed genomic DNA sequences (AB10846-ABL10511), expressed DNA

CC sequences (AB10737-ABL7072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at [ftp://wipo.int/pct/published_pct_sequences](http://wipo.int/pct/published_pct_sequences).

XX

SQ Sequence 593 AA;

Query Match 75.5%; Score 105; DB 22; Length 593;
 Best Local Similarity 64.0%; Pred. No. 8e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 6; Mismatches 3; Sq

1 YQCEIIGKSFSDKSNITRHURHTG 25
 Db 244 YKCDILOGKVFSQKSNLARHHRVHTG 268

Db	445	YQCSVCGKSFADRSNMTLHHLHSG	469
QY	1	YQCBICGKSFSDKNLTMRHRIHTG	25

Search completed: January 6, 2004, 16:10:46
Job time: 43 secs

human prey protein for *Shigella* ospC #2; prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1; *Shigella*; *Shigelloid*; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human. Homo sapiens.

WO200257303-A2.
25-JUL-2002.
11-JAN-2002; 2002WO-EP00777.
12-JAN-2001; 2001US-261130P.
(HYBR-) HYBRIGENICS.
Legrain, P.;
WPI; 2002-599706/64.
N-PSB; ABS5109.

New complex of protein-protein interactions between a bait *Shigella* flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.

Claim 7; Page 137; 162pp; English.

The invention relates to a complex of protein-protein interactions between a *Shigella flexneri* polypeptide (e.g. ospB; ospD1; ipaD; ipaC, ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the *Shigella flexneri* polypeptide and a mammalian polypeptide defined in the specification; (2) selecting a modulating compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID (selected interacting domain) polypeptide or its fragment or variant comprising the human polypeptides appearing as ABG0042; ABG0242; (5) a SID polynucleotide or its fragment or variant comprising encoding the above polypeptides a vector comprising (5); (6) a recombinant host cell containing the vector; and (10) a protein chip comprising *Shigella flexneri* polypeptide and a mammalian polypeptide defined in the specification. A pharmaceutical composition comprising the compound, polypeptide or polynucleotide is useful for treating or preventing shigellosis (bacillary dysentery) in a human or mammal. The present sequence represents a human prey protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a *Shigella* protein.

Sequence 362 AA:

Qy	1	YQEBIGKSFSDKSNLTRHLRHTG	25
Query	YQEBIGKSFSDKSNLTRHLRHTG		
Match		74.8%; Score 104; DB 23;	Length 362;
Best local Similarity		76.0%; Pred No. 6	5e-07;
Matches	19;	Conservative 1;	Mismatches 5;
		Indels 0;	Gaps

GeneCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2004, 16:08:31 ; Search time 36 Seconds
 (without alignments)

179.203 Million cell updates/sec

Title: US-09-774-940A-1
 Perfect score: 139
 Sequence: 1 YQCCHGKRSKDKNLTRHLRHTG 25

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBBL 23;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	106	76.3	555 4 Q9NUR2	Q9nur2 homo sapien
2	106	76.3	561 4 Q96B88	Q96b88 homo sapien
3	105	75.5	587 5 Q9NKB9	Q9nk98 drosophila
4	105	75.5	608 11 Q8VDT8	Q8vdt8 mus musculus
5	105	75.5	608 11 Q8BKW8	Q8bkw8 mus musculus
6	105	75.5	608 11 Q8BKP2	Q8bkp2 mus musculus
7	104	74.8	608 11 Q8R203	Q8r203 mus musculus
8	104	74.8	576 4 Q9EN22	Q9en22 homo sapien
9	104	74.8	606 4 Q9DUJ4	Q9duj4 homo sapien
10	103	74.4	4 Q8NA42	Q8na42 homo sapien
11	102	73.4	106 4 Q9UFH1	Q9ufh1 homo sapien
12	102	73.4	337 11 Q8R0KO	Q8r0ko mus musculus
13	102	73.4	496 11 Q8CG53	Q8c53 mus musculus
14	102	73.4	495 11 Q8BG55	Q8bg55 mus musculus
15	102	73.4	530 4 Q8NA64	Q8na64 homo sapien
16	102	73.4	4 Q9NR94	Q9nr94 homo sapien

RESULT 1				
ID	Q9NUR2	PRELIMINARY;	PRT;	555 AA.
AC	Q9NUR2;			
DT	01-OCT-2000	(Tremblrel. 15, Created)		
DT	01-OCT-2000	(Tremblrel. 15, Last sequence update)		
DT	01-MAR-2003	(Tremblrel. 23, Last annotation update)		
DB	Hypothetical protein FLJ1191.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Placenta;			
RA	Iegai T., Ota T., Hayashi K., Sugiyama T., Otsubi T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Isuji S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Niromiya K., Iwayangi T.,			
RA	'NEDO human cDNA sequencing project.';			
RA	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
EMBL	EMBL: AK002053; BAA2059.1;			
DR	HSSP; P0845; 12NF.			
DR	InterPro; IPR001909; KRAB.			
DR	InterPro; IPR007087; Znf_C2H2.			
DR	Pfam; PF01352; GRAB; 1.			
DR	Pfam; PF00096; Znf_C2H2; 11.			
DR	ProDom; PDO00005; Znf_C2H2; 11.			
DR	SMART; SM00349; KRAB_1.			
DR	SMART; SM00355; Znf_C2H2; 11.			
DR	Prosite; PS05085; KRAB; 1.			
DR	Prosite; PS00028; ZINC_FINGER_C2H2_1; 11.			
DR	Prosite; PS05157; ZINC_FINGER_C2H2_2; 11.			
KW	Hypothetical protein; Metal-binding; Zinc; Zinc-finger.			
SEQUENCE	555 AA; 64101 MW; D355B9B6EB2604 CRC64;			

Query Match 76.3%; Score 106; DB 4; Length 555;
 Best Local Similarity 68.0%; Pred. No. 6.2e-08; Indels 0; Gaps 0;
 Matches 17; Conservative 4; Mismatches 4; DB 0;

QY 1 YQCEIGKGSQDKSNLTRHRIHTG 25
 DB 244 YKCDLQGKVFSQKSNLARHWRVHTG 268

RESULT 2

Q96B88 PRELIMINARY; PRT; 561 AA.
 ID Q96B88; AC 096B88; DT 01-DEC-2001 (TREMBirel, 19, Created)
 DT 01-DEC-2003 (TREMBirel, 19, Last sequence update)
 DT 01-MAR-2003 (TREMBirel, 23, Last annotation update)
 DB Hypothetical protein (Zinc finger protein 37A).
 GN ZNF37A
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]—
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA GUY J., Hearn T., Crosier M., Mudge J., Viggiano L., Koczan D.,
 Thiesen H.J., Bailey J., Horvath J., Eichler E.B., Deloukas P.,
 French L., Rogers J., Bentley D., Jackson M.S.;
 "Genomic sequence and transcriptional profile of the boundary between
 pericentromeric satellites and gene-rich human chromosome arm 10p.";
 Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC —
 C— SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; BC015858; AAC015858.1; --.
 DR EMBL; AJ592195; CAD3733.1; --.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007085; Znf_C2H2_sub.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf_C2H2; 10.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
 DR PROSITE; PS00057; ZINC_FINGER_C2H2_2; 12.
 KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
 KW Zinc-finger.
 SQ SEQUENCE 561 AA; 65417 MW; 068789DC7DA04BC3 CRC64;
 Best Local Similarity 76.3%; Score 106; DB 4; Length 561;
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YQCEIGKGSQDKSNLTRHRIHTG 25
 DB 411 YECNECGKSFSEKSTLTHRLHTG 435

RESULT 3

Q9NK88 PRELIMINARY; PRT; 587 AA.
 ID Q9NK88; Q9VUQ2; AC 09NK88; DT 01-OCT-2000 (TREMBirel, 15, Created)
 DT 01-OCT-2000 (TREMBirel, 15, Last sequence update)
 DT 01-OCT-2000 (TREMBirel, 23, Last annotation update)
 DT 01-MAR-2003 (TREMBirel, 23, Last annotation update)
 DB Hypothetical protein (CG15269 protein).
 GN DSG:DG04926.3 OR CG15269.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydriida; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
 RN [1]—
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
 Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
 Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
 Palazzo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitlaw K.,
 Celinker S., Rubin G.M.;
 "An exploration of the sequence of a 2.9-Mb region of the genome of
 Drosophila melanogaster: the Adh region.";
 RL Genetics 153:179-219(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celinker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
 Butenmoff C., Champé C., Chavez C., Chew M., Ciesiolkia L., Doyle C.M.,
 Farfan D., Galle R., George R.A., Harris N.L., Hoskins R.A.,
 Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Le B.,
 Lewins S., Liu P., Lomotan M.A., Mada P., Moshrefi A.R., Moshrefi M.,
 Nixon K., Pacie B., Park S., Pfeiffer B., Poon L., Sequeira A.,
 Sethi H., Snir E., Svirkas R.R., Wan K.H., Weinburg T., Zhang R.,
 Zieran L., Rubin G.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.H.C., Blazej R.G., Champé M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Abayani A., An H.-J., Andrews P., Pfaffnachko C., Baldwin D.,
 Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 Borková D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cowley S., Dahlke C., Davenport L., Davis P.,
 de Pablo J., Delcher A., Deng Z., Daves P., Dewart D., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin R.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
 Fosler C., Gabelli A.B., Garg S., Gelbart W.M., Glässer K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iwegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.C., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levi-BK A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzzey D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nuskeen D.R., Pacie J.M.,
 Palazzo M.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheele F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 Zheng X.H., Zhong W., Zhong X., Zhou Y., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2188-2195 (2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 Carlson J.W., Center A., Champé C., Davenport L.B., Dietz S.M.,

RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresneak D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez C., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibeagwu C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuovo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Preiffer B., Scheeler F.,
 RA Photaneavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svartka R., Tector C., Tyler D.,
 RA Williams S.M., Zavarei J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of *Drosophila melanogaster* genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]

RP SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hrdlicky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krcmiller L., Marshall B., Millburn G., Rubin G.M., Mungall C.J., Lewis S.E.,
 RA Searle S.M.J., Smith E., Shu S., Smutnicki F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [6]

RP SEQUENCE FROM N.A.

RA Adams M.D., Celinker S.E., Gibbs R.A., Robin G.M., Venter C.J.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [7]

RP SEQUENCE FROM N.A.

RA FlyBase

RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB003412; AAFA4921.1; "-".

DR EMBL; AB003446; AAFA53440.2; "-".

DR EMBL; P15822; IBB0.

DR FlyBase; FBgn0028878; BG:PS04929.3.

DR InterPro; IPR0070887; Znf_C2H2.

DR Pfam; PF00086; zf-C2H2; 8.

DR PROSITE; PS00028; ZINC_FINGER_C2H2; 1; 7.

DR PROSITE; PS00157; ZINC_FINGER_C2H2; 2; 8.

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 587 AA; 63737 MM; 9PC9553688340CD CRC64;

Query Match 75.5%; Score 105; DB 5; Length 587;
 Best Local Similarity 64.0%; Pred. No. 9 4e-08; Indels 0; Gaps 0;
 Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YOCBICGKSFSDKSNTLRLRHTG 25

Db 439 YQCSVCGKSFADRSNMTLHRHMSG 463

RESULT 4

QVDT8 PRELIMINARY; PRT; 608 AA.

ID QVDT8

AC QVDT8;

DT 01-MAR-2002 (TREMBrel. 20, Created)

DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)

DE Similar to zinc finger protein 189.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 -- SUNCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC EMBL; BC021326; ARK21326.1; --.

DR InterPro; IPR001909; KRAB.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR007086; zf-C2H2; sub.

RP SEQUENCE FROM N.A.

RA Pfam; PF01352; KRAB; 1.

DR PFam; PF00096; zf-C2H2; 16.

DR PRINTS; PR00088; ZINC_FINGER.

DR PRODOM; PR000003; Znf_C2H2; 11.

DR SMART; SM00349; KRAB; 1.

DR SMART; SM00355; Znf_C2H2; 16.

DR PROSITE; PS5005; KRAB; 1.

DR PROSITE; PS0028; ZINC_FINGER_C2H2; 1; 16.

DR PROSITE; PS50157; ZINC_FINGER_C2H2; 2; 16.

KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.

SQ SEQUENCE 608 AA; 70548 MM; 4BF6B013D2730A4E CRC64;

Query Match 75.5%; Score 105; DB 11; Length 608;
 Best Local Similarity 76.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;
 Matches 19; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YOCBICGKSFSDKSNTLRLRHTG 25

Db 354 YQCOEGKSFSQLCNLRLRHTG 378

RESULT 5

Q8BK8 PRELIMINARY; PRT; 608 AA.

ID Q8BK8

AC Q8BK8;

DT 01-MAR-2003 (TREMBrel. 23, Created)

DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)

DB Zinc finger protein 189 homolog.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RA The FANTOM Consortium,

RA "Analysis of the mouse transcriptome based on functional annotation of the RIKEN Genome Exploration Research Group Phase I & II Team";

RT NCBITaxID=57;

DR EMBL; AX049475; BAC33769.1; "-".

DR SEQUENCE 608 AA; 70522 MM; 5C07ACT71CBFB3P06 CRC64;

Query Match 75.5%; Score 105; DB 11; Length 608;
 Best Local Similarity 76.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;
 Matches 19; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YOCBICGKSFSDKSNTLRLRHTG 25

Db 354 YQCOEGKSFSQLCNLRLRHTG 378

RESULT 6

Q8KZP2 PRELIMINARY; PRT; 608 AA.

ID Q8KZP2

AC Q8KZP2;

DT 01-MAR-2003 (TREMBrel. 23, Created)

DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)

DB Zinc finger protein 189 homolog.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RA STRAIN=257BL/6J; TISSUE=Dorsal root ganglion;

RA MEDLINE=2234683; Pubmed=12466851;

RA The FANTOM Consortium,

RA "Analysis of the mouse transcriptome based on functional annotation of the RIKEN Genome Exploration Research Group Phase I & II Team";

RT 60,770 full-length cDNAs. ";

RL Nature 420:563-573 (2002);

DR EMBL; AR051265; BAC34582.1; -;

SQ 608 AA; 70522 MW; 862F0214A16BA36F CRC64;

Query Match 75.5%; Score 105; DB 11; Length 608; Best Local Similarity 76.0%; Pred. No. 9.8e-08; Matches 19; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YOCEICGKSFSKSNLTRHLRHTG 25

Db 354 YQCECGKSFSKSNLTRHLRHTG 378

RESULT 7

Q8R2Q3 PRELIMINARY; PRT; 566 AA.

ID Q8R2Q3; AC Q8R2Q3; DT 01-JUN-2002 (TREMBLrel. 21, Created) 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE Similar to KIAA1948 protein

OS Mus musculus (Mouse)

OC Buka-Yvota; Metzca; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;

RN [1]_SEQUENCE FROM N.A.

RA Sträuber R.;

RL Submitted (APR-2002) to the EMBL/genBank/DBJ databases.

DR EMBL; BC057344; AAH07344.1; -;

DR InterPro; IPR011909; KRAB.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF01352; KRAB; 1

DR Pfam; PF00096; zf_C2H2; 10.

DR SMART; SM00349; KRAB; 1.

DR PROSITE; PS50805; Znf_C2H2; 10.

DR PROSITE; PS00058; ZINC_FINGER_C2H2_1; 10.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 10.

DR Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 566 AA; 64569 MW; CC6DC1CE512056D CRC64;

Query Match 74.8%; Score 104; DB 11; Length 566; Best Local Similarity 76.0%; Pred. No. 1.3e-07; Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YOCEICGKSFSKSNLTRHLRHTG 25

Db 251 YDCKECGKSFILKSNLTRHLRHTG 275

RESULT 8

Q9GN22 PRELIMINARY; PRT; 576 AA.

ID Q9GN22; AC Q9GN22; DT 01-DEC-2001 (TREMBLrel. 19, Created) 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DB Hypothetical protein FLJ31526.

OS Homo sapiens (Human).

OC Buka-Yvota; Metzca; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

RN [1]_SEQUENCE FROM N.A.

RA Williams S.;

RL Submitted (AUG-2001) to the EMBL/genBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

AC Q9GN22; DT 01-MAY-2000 (TREMBLrel. 13, Created) 01-OCT-2001 (TREMBLrel. 18, Last sequence update)

DR EMBL; CAB55432.2; -;

DR HSSP; P08047; ISP2.

DR InterPro; IPR011909; KRAB.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR07086; Znf_C2H2_sub.

DR Pfam; PF01352; KRAB; 1.

DR Pfam; PF00096; zf_C2H2; 14.

DR PRINTS; PR00048; ZINC_FINGER.

DR SMART; SM00349; KRAB; 1.

DR SMART; SM00355; KRAB; 1.

DR PROSITE; PS50805; KRAB; 1.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 14.

DR Metal-binding; Nuclear Protein; Zinc; Zinc-finger.

FT NON_TER 1

FT NON_TER 605 606

SQ SEQUENCE 606 AA; 69975 MW; B2C611-019C7B3B CRC64;

Query Match 74.8%; Score 104; DB 4; Length 605; Best Local Similarity 68.0%; Pred. No. 1.4e-07; Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YOCEICGKSFSKSNLTRHLRHTG 25

Db 334 YCEBECGKAFGSSDILTRHLRHTG 358

RESULT 10

Q8NA42

Q8NA42 PRELIMINARY; PRT; 475 AA.
 ID DR PRODOM; PD000003; Znf_C2H2; 2.
 AC DR SMART; SM00355; Znf_C2H2; 3.
 DT DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DT DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 DE KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 OS Homo sapiens (Human).
 OC Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Hotuta T., Hiracka S., Murakawa K., Takiguchi S., Kusano J., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kituchi H., Hama K., Nagai K., Oshima A., Sugiyama A., Nagai T., Isogai T., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Niishikawa T., Nagatsu M., Takahashi-Fujii A., Oshima Y., Nagai K., Isogai T., "NEDO human cDNA sequencing project.", Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RL !- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC EMBL; AK033182; BAC04086_1; InterPro; IPR01399; KRAB; InterPro; IPR007087; Znf_C2H2.
 DR Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR !- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AK033182; BAC04086_1; InterPro; IPR01399; KRAB; InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF01352; KRAB; Pfam; PF00096; zf-C2H2; 10.
 DR PRINTS; PRO0048; ZINC_FINGER.
 DR SMART; SM00349; KRAB; SMART; SM00355; Znf_C2H2; 11.
 DR PROSITE; PS50805; KRAB; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_1; 11.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 11.
 KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 SQ SEQUENCE 475 AA; 54613 MW; 2F47070F5C2E5B2B CRC64;
 Query Match 74.1%; Score 103; DB 4; Length 475;
 Best Local Similarity 72.0%; Pred. No. 1.6e-07; Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YCCEICKFSFSKSNLTRHLRIHTG 25
 Db 422 YCNECKAFAKNCSNLTRHLRIHTG 446

RESULT 11
 Q9UFH1 PRELIMINARY; PRT; 106 AA.
 ID DR PRODOM; PD000003; Znf_C2H2; 2.
 AC DR SMART; SM00355; Znf_C2H2; 3.
 DT DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DT DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 DE KW Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Poustka A., Klein M., Meves H. W., Gassnerhuber J., Wiemann S., Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RC TISSUE=Testis;
 RA TISSUE=Testis;
 RA TISSUE=Testis;
 DR All2078; CAB9253_1; DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2_3.
 DR PRINTS; PRO0048; ZINC_FINGER.

RESULT 12
 Q9UFH1 PRELIMINARY; PRT; 337 AA.
 ID DR PRODOM; PD000003; Znf_C2H2; 2.
 AC DR SMART; SM00355; Znf_C2H2; 3.
 DT DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DT DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 DE KW Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC02676; AAH2676_1; InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 8.
 DR SMART; SM00355; Znf_C2H2; 8.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
 KW Metal-Binding; Zinc; Zinc-finger.
 SQ SEQUENCE 337 AA; 37455 MW; C0054DAL1A98C312 CRC64;
 Query Match 73.4%; Score 102; DB 11; Length 337;
 Best Local Similarity 64.0%; Pred. No. 1.6e-07; Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

RESULT 13
 Q8C5G3 PRELIMINARY; PRT; 496 AA.
 ID DR PRODOM; PD000003; Znf_C2H2; 2.
 AC DR SMART; SM00355; Znf_C2H2; 3.
 DT DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DT DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
 DE KW Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE=Genad; MEDLINE=22354683; PubMed=12466851;
 RA The RANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2004, 16:05:21 ; search time 11 Seconds
 (without alignment(s))

106.879 Million cell updates/sec

Title: US 09-774-940A1
 Perfect score: 139
 Sequence: 1 YQCICIGKSFSDKSNLTHLRIHNG 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	106	76.3	242	1 Z37A_HUMAN	P17032 homo sapien
2	104	74.8	626	1 Z189_HUMAN	075820 homo sapien
3	102	73.4	803	1 Z226_HUMAN	09ny6 homo sapien
4	102	73.4	803	1 Z226_HUMAN	09ju3 homo sapien
5	101	72.7	485	1 Z165_HUMAN	P49910 homo sapien
6	101	72.7	576	1 Z431_HUMAN	08tf32 homo sapien
7	100	71.9	247	1 Z273_HUMAN	014593 homo sapien
8	100	71.9	595	1 ZN85_HUMAN	Q03923 homo sapien
9	100	71.9	1191	1 ZN91_HUMAN	Q05481 homo sapien
10	99	71.2	348	1 Z134_HUMAN	P52741 homo sapien
11	98	70.5	169	1 ZF58_MOUSE	P16372 mus musculus
12	98	70.5	473	1 ZF38_HUMAN	Q9Y5A6 homo sapien
13	98	70.5	555	1 ZP_8_MOUSE	Q9Y2P7 homo sapien
14	98	70.5	604	1 GLAS_DROME	Q07231 mus musculus
15	98	70.5	683	1 Z226_HUMAN	P13360 drosophila
16	98	70.5	683	1 Z226_HUMAN	014978 homo sapien
17	97	69.8	406	1 Z333_HUMAN	0961w9 homo sapien
18	97	69.8	810	1 Z33A_HUMAN	Q06730 homo sapien
19	96	69.1	216	1 Z434_HUMAN	Q9nx65 homo sapien
20	96	69.1	275	1 Z223_HUMAN	Q75346 homo sapien
21	96	69.1	325	1 ZN36_HUMAN	P17029 homo sapien
22	96	69.1	367	1 Z211_HUMAN	Q13398 homo sapien
23	96	69.1	424	1 ZFPI_MOUSE	P08042 mus musculus
24	96	69.1	469	1 Z135_HUMAN	P52742 homo sapien
25	96	69.1	489	1 ZN71_HUMAN	Q9nqz8 homo sapien
26	96	69.1	574	1 YEF3_HUMAN	Q9p255 homo sapien
27	96	69.1	643	1 ZN23_HUMAN	P17027 homo sapien
28	96	69.1	803	1 ZM33_HUMAN	P17038 homo sapien
29	96	68.3	379	1 Z11B_HUMAN	Q06732 homo sapien
30	95	68.3	428	1 ZN33_HUMAN	P51522 homo sapien
31	95	68.3	738	1 ANX4_HUMAN	P51523 homo sapien
32	94	67.6	56	1 ZN25_HUMAN	P17030 homo sapien
33	94	67.6	292	1 OZF_HUMAN	P28151 bovis tauri

ALIGNMENTS

34	94	57.6	292	1 OZF_HUMAN	Q15072 homo sapien
35	94	67.6	301	1 Z11A_HUMAN	P7013 homo sapien
36	94	67.6	394	1 Z220_HUMAN	P8182 homo sapien
37	94	67.6	457	1 Z140_HUMAN	P2738 homo sapien
38	94	67.6	534	1 Z397_HUMAN	Qnf99 homo sapien
39	94	67.6	616	1 ZN93_HUMAN	P35789 homo sapien
40	94	67.6	671	1 Z282_HUMAN	Qduv7 homo sapien
41	94	67.6	734	1 ZN42_HUMAN	P28698 homo sapien
42	94	67.6	783	1 ZF25_HUMAN	Q1615 homo sapien
43	94	67.6	839	1 Z347_HUMAN	P06se1 homo sapien
44	93	66.9	347	1 ZFP2_MOUSE	P8043 mus musculus
45	93	66.9	364	1 Z430_MOUSE	Q9h891 homo sapien

KW	nuclear transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
FT	non TIER 1
FT	NON TIER 1
FT	ZN_FING 8 30 C2H2-TYPE
FT	ZN_FING 36 58 C2H2-TYPE
FT	ZN_FING 64 86 C2H2-TYPE
FT	ZN_FING 92 114 C2H2-TYPE
FT	ZN_FING 120 142 C2H2-TYPE
FT	ZN_FING 148 170 C2H2-TYPE
FT	ZN_FING 176 198 C2H2-TYPE
FT	ZN_FING 204 226 C2H2-TYPE
SQ	SEQUENCE 242 AA: 27810 MN: 2B10451B2ASDAD8 CRC64: 92 YECNCBGSFSEKSTLTKHRLRTHG 116
Db	Query Match 76.3%; Score 105; DB 1; Length 242; Best Local Similarity 72.0%; Pred. No. 1.4e-08; Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Qy 1 YQCEIIGGSFSDISNLTRHRLRTHG 25
Qy	1 YQCEIIGGSFSDISNLTRHRLRTHG 25
Db	92 YECNCBGSFSEKSTLTKHRLRTHG 116
RESULT 2	
Z189_HUMAN	
ID 2189_HUMAN	
STANDARD; PRT; 626 AA.	
AC 075820; OT7802; Q9UBL4; Q9UEP9; Q9UPF0; Q9UPF1;	
DT 15-DEC-1998 (Rel. 37, Created)	
15-DEC-1998 (Rel. 37, Last sequence update)	
DT 15-SEP-2003 (Rel. 42, Last annotation update)	
DE Zinc finger protein 189.	
GN ZNF189.	
OS Homo sapiens (Human).	
OC Burkayrta; Metaxoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]-	
RP SEQUENCE FROM N. A. (ISOFORMS 1, 2, 3 AND 4).	
RC TISSUE-Bone marrow; MEDLINE=9817535; PubMed=9653648;	
RX MEDLINE=9817535; PubMed=9653648;	
RA Odeberg J., Roedig O., Gudmundson G., Ahmadian A., Roshani L.,	
RA Williams C., Larsson C., Ponten F., Uhlen M., Rasheim H.-C.,	
RA Lundberg J.; characterization of ZNF189, a novel human Kruppel-like	
RT zinc finger gene localized to chromosome 9q22-q31.;"	
RL Genomics 50:213-221(1998).	
RN [2]-	
RP SEQUENCE FROM N. A. (ISOFORMS 1 AND 4).	
RX MEDLINE=99346145; PubMed=1415358;	
RA Odeberg J., Ahmadian A., Williams C., Uhlen M., Ponten F.,	
RA Lundberg J.;	
RT "Context-dependent tag-polymerase-mediated nucleotide alterations, as	
RT revealed by direct sequencing of the ZNF189 gene: implications for	
RT mutation detection.;"	
RL Gene 235:103-109(1999).	
CC -!- FUNCTION: May function as a transcription factor.	
CC -!- FUNCTION: May function as a transcription factor.	
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).	
CC -!- ALTERNATIVE PRODUCTS: Named isoforms=4;	
CC -!- Event=Alternative splicing; Named isoforms=4;	
CC -!- Name=;	
CC -!- IsoId=075820-1; Sequence=Displayed;	
CC -!- Name=;	
CC -!- IsoId=075820-2; Sequence=vsp_006900;	
CC -!- Name=3; Synonyms=B2;	
CC -!- IsoId=075820-3; Sequence=vsp_006901;	
CC -!- Name=4;	
CC -!- IsoId=075820-4; Sequence=vsp_006899;	
CC -!- TISSUE SPECIFICITY: Ubiquitous;	
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.	
CC -!- SIMILARITY: Contains 1 KRAB domain.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC CC CC CC CC CC

DR EMBL; U95992; AAC25910.1; -

DR EMBL; U95991; AAC25909.1; -

DR EMBL; U75454; AAC33978.1; -

DR EMBL; AF025770; AAC33799.1; -

DR EMBL; AF025771; AAC33800.1; -

DR EMBL; AF025772; AAC30527.1; -

DR EMBL; AF025772; AAD50528.1; -

DR HSSP; P0847; ISP2; ZNF189.

DR Genew; HGNC;12980; ZNF189.

DR MIM; 603132; -

DR GO; GO:0003700; P:transcription factor activity; TAS.

DR GO; GO:0003222; P:negative regulation of transcription from P. . . ; TAS.

DR InterPro; IPR01909; KRAB.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR007086; Znf_C2H2_sub.

DR PFam; PF01352; KRAB; 1.

DR PFam; PF00196; ZF_C2H2; 15.

DR PRINTS; PR00048; ZINFPINGER.

DR PRODOM; PDD00003; Znf_C2H2; 11.

DR SMART; SM00349; KRAB_1.

DR SMART; SM00355; Znf_C2H2; 16.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 16.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 16.

KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;

KW Nuclear protein; Repeat; Alternative splicing.

FT DOMAIN 14 89 KRAB.

FT ZN_FING 148 170 C2H2-TYPE.

FT ZN_FING 176 198 C2H2-TYPE.

FT ZN_FING 204 226 C2H2_TYPR.

FT ZN_FING 232 254 C2H2-TYPE.

FT ZN_FING 260 282 C2H2-TYPE.

FT ZN_FING 288 310 C2H2-TYPE.

FT ZN_FING 316 338 C2H2-TYPE.

FT ZN_FING 344 366 C2H2-TYPE.

FT ZN_FING 372 394 C2H2-TYPE.

FT ZN_FING 400 422 C2H2-TYPE.

FT ZN_FING 456 478 C2H2-TYPE.

FT ZN_FING 484 506 C2H2-TYPE.

FT ZN_FING 512 534 C2H2-TYPE.

FT ZN_FING 540 562 C2H2-TYPE.

FT ZN_FING 568 590 C2H2-TYPE.

FT ZN_FING 599 621 C2H2-TYPE.

FT VARSPPLIC 1 42 Missing (in isoform 4). /FTId=VSP_006999.

FT VARSPPLIC 12 25 Missing (in isoform 2). /FTId=VSP_006900.

FT VARSPPLIC 1 95 Missing (in isoform 3). /FTId=VSP_006901.

FT CONFLICT 588 588 M->K (IN REF. 2).

SQ SEQUENCE 626 AA; 72978 MW; C110F9943F15BB6 CRC64;

Query Match 74.8%; Score 104; DB 1; Length 626;

Best Local Similarity 76.0%; Pred. No. 7.3e-08; Matches 19; Conservative 1; Mismatches 5; Index 0; Gaps 0;

Matches 19; Conservative 1; Mismatches 5; Index 0; Gaps 0;

QY 1 YQCEICGKSFSKSNITRHLRIHTG 25

QY 1 YQCEICGKSFSKSNITRHLRIHTG 25

Db 372 YQCEICGKSFSKSNITRHLRIHTG 396

DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Zinc finger protein 225.
 GN ZNF226.
 OS Homo sapiens (Human).
 OC Bukarycova; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shannon M., Branscomb B., Hauser L., Gordon L., Ashworth L.,
 RA Stubb L.;
 RT "differential expansion of homologous zinc-finger gene families in
 human chromosome 19q13.2 and mouse chromosome 7.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kvikstad E., Gordon L., Shannon M., Brower A.S., Olsen A.S., Smith L.M.;
 RT "sequence analysis of a 1MB region in 19q13.2 containing a zinc finger
 gene cluster.;"
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H., Smith L.M.;
 RA Nagatsuma M., Hocicri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba S., Iishi Y., Murakawa S., Murakami K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Niromiwa K., Iwayanagi T.;
 RA "NEDO human cDNA sequencing project.;"
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RX MEDLINE=22398257; PubMed=12477932;
 RA Straubinger R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schulier G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scarpa M.B., Bandal M.F., Casavant T.L., Schatz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueline N.A., Peters J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:6899-16903 (2002).
 CC -- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -- SUBCELLULAR LOCATION: Nucleus (Probable).
 CC -- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
 CC -- SIMILARITY: Contains 1 KRAB domain.
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 DR AC07431; AAF8103;
 DR EMBL; AK023091; BAB43981;
 DR -----
 DR EMBL; BC024197; AAH24197.1; -.
 DR HSSP; P08047; ISP2.
 DR Gene3D; HGENC;31019; ZNF226.
 DR InterPro; IPR01909; KRAB.
 DR InterPro; IPR07087; ZNF_C2H2.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 1B.
 DR ProDom; PD000003; Znf_C2H2; 15.
 DR SMART; SM00345; KRAB; 1.
 DR PROSITE; PS50805; Znf_C2H2; 18.
 DR PROSITE; PS50028; ZINC_FINGER_C2H2_1; 17.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 19.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein.
 FT DOMAIN 8 78 KRAB.
 FT ZN_FING 252 274 C2H2-TYPE (DEGENERATE).
 FT ZN_FING 307 329 C2H2-TYPE.
 FT ZN_FING 335 357 C2H2-TYPE.
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CC	or send an email to licensed@isb-sib.ch).
CC	EMBL: X78932; CAA5532.1; -.
DR	PIR: S47070; S47070.
DR	HSSP: P09047; SP2.
DR	SMART: SM0355; Znf_C2H2; 6.
DR	PROSTRE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR	PROSTE; PS05157; ZINC_FINGER_C2H2_2; 9.
KW	Transcription regulation; DNA-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat.
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FT	ZN_FING <1 19 C2H2-TYPE.
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FT	ZN_FING 53 75 C2H2-TYPE.
FT	ZN_FING 81 102 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 108 130 C2H2-TYPE.
FT	ZN_FING 136 158 C2H2-TYPE.
FT	ZN_FING 164 186 C2H2-TYPE.
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FT	ZN_FING 220 242 C2H2-TYPE (ATYPICAL).
SQ	247 AA; 28448 MW; 5AB5B6F46C3234E2 CRC64;
Query	Match 71.9%; Score 100; DB 1; Length 247;
Best	Local Similarity 68.0%; Prev. No. 1.1e-07;
Matches	17; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Gaps
QY	1 YC0ECCGKSVDKSNTRHURIRHG 25
Db	192 YKCEEEGKAFNRSSNLTRHKKIHG 216
RESULT 8	
ZN85_HUMAN	STANDARD; PRT: 595 AA.
ID	
AC	Q03933;
DT	01-OCT-1994 (Rel. 29, Created)
DT	15-SEP-2003 (Rel. 42, last annotation update)
DB	Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1).
GN	ZN85.
OS	Homo sapiens (Human).
OC	Bukay-Yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID:9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC	TISSUE=Placenta;
RX	MEDLINE=9905337; PubMed=9939802;
RA	Poncelet D.A., Belleroiod E.J., Bastiaens P.V., Demoitie M.A.,
RA	Marine J.C., Pendeville H., Alami Y., Devos N., Lecocq P.J., Ogawa T.,
RA	Muller M., Martial J.A.,
RT	"Functional analysis of ZN85 KRAB zinc finger protein, a member of the highly homologous ZNF91 family.;"
RT	DNA Cell Biol. 17:931-943(1998).
RN	[2]
RP	SEQUENCE OF 1-196 FROM N.A.
RX	MEDLINE=9219451; PubMed=2023909;
RA	Belleroiod E.J., Poncelet D.A., Lecocq P.J., Revelant O.,
RA	Martial J.A.,
RT	"The evolutionarily conserved Kruppel-associated box domain defines a subfamily of eukaryotic multifingered proteins;"
RT	Proc. Natl. Acad. Sci. U.S.A. 88:3608-3612(1991).
CC	- FUNCTION: TRANSCRIPTIONAL REPRESSOR.
CC	- SUBCELLULAR LOCATION: Nuclear.

CC - I TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN TESTICULAR TISSUES.
 CC - I- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING EMBRYONIC DEVELOPMENT

OPMENT.

ZN₉-HUMAN
 ID_ZN9_HUMAN STANDARD; PRT; 1191 AA.
 AC Q05481; 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DB Zinc finger protein 91 (Zinc finger protein Hfp10) (HFP7).
 GN ZNF91.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9322677; PubMed=8467795;
 RA Bellefroid E.J., Marine J.C., Ried T., Lecocq P.J., Riviere M., Amemiya C.T., Poncelet D.A., Coulie P.G., de Jong P.J., Spirer C., Ward D.C., Marini J.A., "Clustered organization of homologous KRAB zinc-finger genes with enhanced expression in human T lymphoid cells.",; EMBO J. 12:1363-1374 (1993).
 RN [2]
 RP SEQUENCE OF 15-204 FROM N.A.; Published=2003-09-09;
 RA Bellefroid E.J., Poncelet D.A., Decoq P.J., Revelant O., Marini J.A.;
 RA "The evolutionarily conserved Kruppel-associated box domain defines a subfamily of eukaryotic multifingered proteins.",; Proc. Natl. Acad. Sci. U.S.A. 80:3603-3612 (1993).
 CC --!- SUBCELLULAR LOCATION: Nuclear: Nuclear
 CC --!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
 CC --!- SIMILARITY: Contains 1 KRAB domain.
 CC --!- CAUTION: THE SEQUENCE FROM POSITION 1159 TO THE C-TERMINAL IS DERIVED FROM THE TRANSITION OF AN ALU REPEAT.
 CC
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 DR EMBL; M61871; AA08672.1; ALT_SEQ.
 DR PIR; S55305; S35305.
 DR HSP; 208047; 15P2.
 DR GENB; HGNC:13166; ZNF91.
 DR MIM: 603971; --!- GO; GO:0005634; C-nucleus; NAS.
 DR GO; GO:0003700; F:transcription factor activity; NAS.
 DR GO; GO:0008210; Zinc ion binding activity; NAS.
 DR InterPro; IPR01099; KRAB.
 DR InterPro; IPR007087; Zinc finger.
 DR Pfam; PF00152; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 34.
 DR PRINTS; PR00048; ZINCTINGER.
 DR PRINTS; PR00003; ZNF_C2H2; 20.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; Zinc_C2H2; 33.
 DR PS0805; PS0028; Zinc_FINGER_C2H2_1; 31.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 35.
 DR Transcription_finger; Zinc_finger; DNA-binding; Metal-binding; Nuclear protein; Repeat.
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 FT ZN_FING 1134 1156 C2H2-TYPE.
 FT ZN_FING 1191 AA; 13725 MW; 581056BB1B8716D CRC64; SQ SEQUENCE
 Query Match 71.9%; Score 100; DB 1; Length 1191;
 Matches 17; Conservativeness 68.0%; Pred. No. 5; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 YKCEBQGRAFQSSTLTRTRMHG 25
 Db 994 YKCEBQGRAFQSSTLTRTRMHG 1018

RESULT 10
 ZN₉-HUMAN
 ID_ZN9_HUMAN STANDARD; PRT; 348 AA.
 AC P52741; 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DB Zinc finger Protein 134.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Insulinoma.
 RX MEDLINE=95044430; PubMed=7557990;
 RA Tommerup N, Vissing H.;
 RT "Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identify putative candidate genes for developmental and malignant disorders.",
 RT Genomics 27:259-264 (1995).
 CC --!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
 CC --!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC --!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

CC
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DR EMBL; U09412; AAC50233.1; -.

DR PIR; I38599; I38599.

DR HSSP; P0047; SP2; ZNF134.

DR MIM; 604076; -.

GO; GO:0005634; C:nucleus; NAS.

GO; GO:0003700; F:transcription factor activity; NAS.

DR GO:0006355; P:regulation of transcription, DNA-dependent; Nas.

DR InterPro; IPR00787, Znf_C2H2.

DR Pfam; PF00096; zf-C2H2; 9.

DR ProDom; PDD000003; Znf_C2H2; 9.

DR SMART; SM00355; Znf_C2H2; 9.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 9.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 9.

KW transcription regulation; Zinc-finger; DNA-binding; Metal-binding;

KW Nuclear protein; Repeat.

FT ZN_FINGER 97 119 C2H2-TYPE.

FT ZN_FINGER 125 147 C2H2-TYPE.

FT ZN_FINGER 153 175 C2H2-TYPE.

FT ZN_FINGER 181 203 C2H2-TYPE.

FT ZN_FINGER 209 231 C2H2-TYPE.

FT ZN_FINGER 237 259 C2H2-TYPE.

FT ZN_FINGER 265 287 C2H2-TYPE.

FT ZN_FINGER 293 315 C2H2-TYPE.

FT ZN_FINGER 321 343 C2H2-TYPE.

SQ SEQUENCE 348 AA; 40297 MW; E0941AD233EC8670 CRC64;

Query Match 71.2%; Score 99; DB 1; Length 348;

Best Local Similarity 68.0%; Pred. No. 2.2e-07;

Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YQCEIIGKSFSDKSNVTRHLRIHTG 25

Db 153 YECSBGKTPSRKDNTQHKRHTG 177

RESULT 11

ID ZF58_MOUSE STANDARD; PRT; 169 AA.

ID ZF58_MOUSE STANDARD; PRT; 169 AA.

AC P16372;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last Sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Zinc-finger protein 58 '(Zfp-58)' (Zinc finger protein Mfg-1) (FRAGMENT).

DE ZFP58 OR MFG-1.

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murine;

OC NCBITaxonID=10930;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=CD-1; TISSUE=Skeletal muscle;

RX MEDLINE=90083218; PubMed=2512579;

RA Passananti C.; Peluso A.; Caruso M.; Amati P.;

RT "Mouse genes coding for 'zinc-finger'-containing proteins: characterization and expression in differentiated cells.;"

RT Proc. Natl. Acad. Sci. U.S.A. 86:9117-9121(1989).

!- FUNCTION: MAY HAVE A ROLE DURING DIFFERENTIATION PROCESSES.

!- SUBCELLULAR LOCATION: Nuclear (probable).

-! TISSUE SPECIFICITY: LIVER; TESTIS; AND AT CONSIDERABLY LOWER LEVELS IN BRAIN; SPLEEN; HEART.

!- DEVELOPMENTAL STAGE: EXPRESSION IS POSITIVELY REGULATED UPON DIFFERENTIATION, AND IS NOT RELATED TO THE CELL CYCLE.

-! SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

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 or send an email to license@isb-sib.ch).

CC EMBL; M28513; AAA9531.1; -
 DR PIR; A3940; A3940.
 DR HSSP; P25490; 1UBD.
 DR MGD; MGI:99205; ZIFP58.
 DR InterPro; IPR007087; ZIF_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF00096; zf-C2H2_6.
 DR PRINTS; PR0008; ZINC_FINGER.
 DR SMART; SM0035; Znf_C2H2_6.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
 DR PROSITE; PS00517; ZINC_FINGER_C2H2_2; 6.
 DR ZINC-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein.
 FT NON_TER 1
 FT ZN_FING 8 30 C2H2-TYPE.
 FT ZN_FING 36 58 C2H2-TYPE.
 FT ZN_FING 64 86 C2H2-TYPE.
 FT ZN_FING 92 114 C2H2-TYPE.
 FT ZN_FING 120 142 C2H2-TYPE.
 FT ZN_FING 148 >169 C2H2-TYPE.
 FT NON_TER 169 169 C2H2-TYPE.
 SQ 169 AA; 19585 MW; 7F5556B1406CDA3 CRC64;

Query Match 70.5%; Score 98; DB 1; Length 169;
 Best Local Similarity 68.0%; Pred. No. 1 4e-05; Indels 0; Gaps 0;
 Matchers 17; Conservative 3; Mismatches 5;

Qy	Db
1 YCCEBEGKRFSTSSNLSEKRRHTG	25
92 YCCEBEGKRFSTSSNLSEKRRHTG	116

RESULT 12

ZFP38_HUMAN
 ID ZFP38_HUMAN STANDARD; PRT; 473 AA.
 AC Q9YK46; O9H0B5; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-SEP-2003 (Rel. 41, Last annotation update)
 DE Zinc finger Protein 38 homolog (Zfp-38) (NY-REN-21 antigen).
 GN ZFP38.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE= testis
 RX MEDLINE:2115917; PubMed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassehuber J., Glassl S.,
 RA Ansorge W., Boecker M., Bloecker H., Bayersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Kocher K., Strack N.,
 RA Mewes H.-W., Ottewaldler B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poussika A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 analysis of 500 novel complete protein coding human cDNAs.";
 RT Genome Res. 11:422-435(2001).
 RN [2]
 RP SEQUENCE OF 62-473 FROM N.A.
 RC TISSUE=renal cell carcinoma;
 RX MEDLINE:9418124; PubMed=10508479;
 RA Scamian M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H.,
 RA Jongeneel C.V., Gure A.O., Jager D., Jager E., Kauth A., Chen Y.-T.,
 RA Old L.J.;
 RT "Antigens recognized by autologous antibody in patients with renal-
 cell carcinoma.";
 RT Int. J. Cancer 83:456-464(1999);

CC -!- FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: nuclear (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
 CC -!- SIMILARITY: Contains 7 C2H2-type zinc fingers.
 CC
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 CC
 EMBL; ALL36865; CAB66799.1; -.
 EMBL; AP155100; AAD42866.1; -.
 EMBL; GO0005334; C:nucleus; NAS.
 GO; GO0015633; P:transcriptional activator activity; NAS.
 GO; GO0006355; P:regulation of transcription, DNA-dependent; NAS.
 InterPro; IPR003309; Treg-SCAN.
 InterPro; IPR000787; Znf_C2H2.
 InterPro; IPR002033; SCAN; 1.
 Pfam; PF00096; zf-C2H2; 7.
 Prodom; PD000003; Znf_C2H2; 7.
 SMART; SM00355; Znf_C2H2; 7.
 PROSITE; PS50804; SCAN_BOX; 1.
 PROSITE; PS50028; ZINC_FINGER_C2H2; 1; 6.
 DR PROSITE; PS01017; ZINC_FINGER_C2H2; 7.
 DR Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; KW Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; KW
 Transcription regulation; Activator.
 FT DOMAIN 45 127 SCAN_BOX.
 FT ZN_FING 277 299 C2H2-TYPE 1.
 FT ZN_FING 305 327 C2H2-TYPE 2.
 FT ZN_FING 333 354 C2H2-TYPE 3.
 FT ZN_FING 360 382 C2H2-TYPE 4.
 FT ZN_FING 388 410 C2H2-TYPE 5.
 FT ZN_FING 416 438 C2H2-TYPE 6.
 FT ZN_FING 444 466 C2H2-TYPE 7.
 SQ 473 AA; 53658 MW; D9A26694B114B96F CRC64;

RESULT 13
 2256_HUMAN STANDARD; PRT; 474 AA.
 AC Q9Y2P7; Q9BW71; .
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein 256 (Bone marrow zinc finger 3) (BMZF-3).
 GN BMZF3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=bone marrow;
 RX MEDLINE=2005457; PubMed=1585455;
 RA Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., He K.-L.,
 RA RA Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z.,
 RT "Molecular cloning of six novel Kruppel-like zinc finger genes from
 hematopoietic cells and identification of a novel transregulatory

RT domain KRNB.";
 RL J. Biol. Chem. 274:35741-35748(1999).
 RN [2] SEQUENCE FROM N.A.
 RP TISSUE=placenta;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmeh C.M., Schuler G.D.,
 RA Altchuk S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S.A., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Farhy J., Heaton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Snailus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; Gay L.J., Hulyk S.W.,
 RA human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -!- FUNCTION: NAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: BELONGS TO THE KRUEPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
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 CC
 EMBL; AP067165; AAD3249.1; -.
 DR PRODOM; PD000003; Znf_C2H2; 12.
 DR SMART; SM00355; Znf_C2H2; 14.
 DR PROSITE; PS50028; ZINC_FINGER_C2H2; 1; 14.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2; 2; 14.
 DR KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat.
 FT ZN_FING 86 108 C2H2-TYPE.
 FT ZN_FING 114 136 C2H2-TYPE.
 FT ZN_FING 142 164 C2H2-TYPE.
 FT ZN_FING 170 192 C2H2-TYPE.
 FT ZN_FING 198 220 C2H2-TYPE.
 FT ZN_FING 226 248 C2H2-TYPE.
 FT ZN_FING 254 276 C2H2-TYPE.
 FT ZN_FING 282 304 C2H2-TYPE.
 FT ZN_FING 310 332 C2H2-TYPE.
 FT ZN_FING 338 360 C2H2-TYPE.
 FT ZN_FING 366 388 C2H2-TYPE.
 FT ZN_FING 394 416 C2H2-TYPE.
 FT ZN_FING 422 444 C2H2-TYPE.
 FT ZN_FING 450 472 C2H2-TYPE.
 FT COMPFLICT 421 421 L->P (IN REF. 2).
 SQ SEQUENCE FROM N.A.
 Query Match 70.5%; Score 98; DB 1; Length 474;
 Best Local Similarity 68.0%; Pred. No. 4.3e-07;

Matches	17; Conservative	2; Mismatches	6; Indels	0; Gaps	0;
QY	1 YOCEIGGKSISDKSNTLTHRIHRTG 25				
Db	422 YECSEGGKSISQSSNTLNHRIHSG 445				
RESULT 14					
ZFP38	MOUSE	STANDARD;	PRT;	555 AA.	
ID					
AC	Q07231;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	15-SEP-2000 (Rel. 42, Last annotation update)				
DE	Zinc finger protein 38 (ZFP-38) (CTF151) (Transcription factor RU49).				
GN					
OS	Mus musculus (Mouse)				
OC	Bukar-Yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX					
NCBI_TAXID	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CB7BL/6;				
RX	MEUDINE93183157; PubMed=1214028;				
RA	Chowdhury K.;				
RT	"The ubiquitous transactivator ZFP-38 is upregulated during and oocytes during meiosis.";				
RL	Dev. Biol. 153:356-367(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CB7BL/6;				
RX	MEUDINE93183157; PubMed=86225807;				
RA	Yang X.W., Zhong R., Heintz N.;				
RT	"Granule cell specification in the developing mouse brain as defined by expression of the zinc finger transcription factor RH49.";				
RL	Development 122:55-56(1995).				
CC	FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR. ASSOCIATED WITH MEIOSIS IN BOTH MALE AND FEMALE GAMETOGENESIS. MAY HAVE DIFFERENT FUNCTIONS IN SOMATIC CELLS.				
CC	- - SUBCELLULAR LOCATION: NUCLEAR.				
CC	- - TISSUE SPECIFICITY: PREDOMINANTLY IN THE SPERMATOCYTES AND SPERMATIDS OF ADULT TESTES. IT IS ALSO PRESENT AT LOWER LEVELS IN THE OVARY, BRAIN, SPLEEN, EMBRYO AND FETUS.				
CC	- - DEVELOPMENTAL STAGE: FIRST DETECTED BETWEEN 2 AND 3 WEEKS AFTER BIRTH. IN PARALLEL WITH THE ONSET AND PROGRESSION OF MEIOSIS. IT IS EXPRESSED DURING OOGENESIS FROM THE PACHYTE STAGE OF MEITIC PROPHASE THROUGH TO POSTMEIOTIC CELLS.				
CC	- - SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.				
CC	- - SIMILARITY: Contains 1 SCAN box domain.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).				
DR	EMBL; D10630; BAA01480.1; -				
DR	EMBL; X63747; CAA5280.1; -				
DR	EMBL; U01671; AAB03786.1; -				
DR	PIR; A55560; A56550.				
DR	HSSP; P08845; I2NPF.				
DR	MGD; MGI:991182; Zipro1.				
DR	InterPro; IPR003309; Treg SCAN.				
DR	Int-EP-PRO; IPR007087; Znf_C2H2.				
DR	Pfam; PF02023; SCAN_1.				
DR	Pfam; PF00096; zf-C2H2; 7.				
DR	ProDom; PD00003; Znf_C2H2; 6.				
DR	SMART; SM00431; LER_1.				
DR	SMART; SM00355; Znf_C2H2; 7.				
DR	PROSITE; PS00058; SCAN BOX_1.				
DR	PROSITE; PS00157; ZINC_FINGER_C2H2_1; 7.				
KW	Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; Developmental protein; Spermatogenesis; Transcription regulation; Activator.				
FT	DOMAIN 18 134 3 X 39 AA APPROXIMATE TANDEM REPEATS.				
FT	REPEAT 18 56 1-1.				
FT	REPEAT 96 134 1-3.				
FT	REPEAT 122 204 SCAN BOX.				
FT	ZN_FING 381 C2H2-TYPE.				
FT	ZN_FING 387 C2H2-TYPE.				
FT	ZN_FING 415 C2H2-TYPE.				
FT	ZN_FING 464 C2H2-TYPE.				
FT	ZN_FING 470 C2H2-TYPE.				
FT	ZN_FING 498 520 C2H2-TYPE.				
FT	ZN_FING 548 548 C2H2-TYPE.				
FT	CONFLICT 193 193 T -> A (IN REF. 2 AND 3).				
FT	CONFLICT 216 216 N -> S (IN REF. 3).				
FT	CONFLICT 234 234 S -> P (IN REF. 3).				
FT	CONFLICT 334 347 ASTQDTGSKRGAEP -> PLFKTQVPGRRGA (IN REF. 3).				
FT	CONFLICT 401 402 NL -> KV (IN REF. 3).				
FT	CONFLICT 478 478 S -> E (IN REF. 3).				
FT	CONFLICT 495 495 Z -> K (IN REF. 2).				
FT	CONFLICT 507 507 F -> L (IN REF. 2).				
FT	CONFLICT 510 510 S -> N (IN REF. 2).				
SO	SEQUENCE 555 AA; 63042 MW; C1E8BPA0119C6C6 CRC64;				
QY	1 YOCEIGGKSISDKSNTLTHRIHRTG 25				
Db	442 YOCCDGKAFSGKGSLSLRHRTG 466				
RESULT 15					
ID	GLAS_DROME	STANDARD;	PRT;	604 AA.	
AC	P13370;				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Glass protein.				
GN	GL.				
OS	Drosophila melanogaster (Fruit fly)				
OC	Bukar-Yota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriidae; Drosophilidae; Drosophila.				
OC	NCBI_TAXID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEUDINE89365138; PubMed=2770860;				
RA	Moses K., Ellis M.C., Rubin G.M.;				
RT	"The glass gene encodes a zinc-finger protein required by Drosophila photoreceptor cells."				
RT	Nature 340:531-536(1999).				
CC	- - FUNCTION: GLASS IS PROBABLY A TRANSCRIPTION FACTOR REQUIRED FOR GENE EXPRESSION SPECIFIC TO PHOTORECEPTOR CELLS.				
CC	- - SUBCELLULAR LOCATION: Nuclear (Potential).				
CC	- - SIMILARITY: Contains 5 C2H2-type zinc fingers.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				

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 CC or send an email to license@isb-sib.ch).

DR EMBL; X11400; CAA33450.1; -
 DR PIR; S05447; S05447; -
 DR HSSP; P08046; 1A1I.
 DR TRANSFAC; T00329; -
 DR Flybase; FBgn0004618; g1.

DR GO; GO:000534; C:nucleus; IDA.
 DR GO; GO:0007459; P:photoreceptor commitment (sensu Drosophila); IMP.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf_C2H2; 5.
 DR PRODOM; PD00003; Znf_C2H2; 2.
 DR SMART; SM0355; Znf_C2H2; 5.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
 DR Transcription; regulation; Zinc-finger; Metal-binding; DNA-binding;

KW Repeat; Vision; Nuclear protein.
 FT ZN_FING 437 459 C2H2-TYPE 1.
 FT ZN_FING 465 487 C2H2-TYPE 2.

FT ZN_FING 493 515 C2H2-TYPE 3.
 FT ZN_FING 521 543 C2H2-TYPE 4.
 FT ZN_FING 549 571 C2H2-TYPE 5.

FT VARIANT 60 60 E -> Q.
 FT VARIANT 351 362 PM -> SL.
 FT VARIANT 377 377 S -> T.

SQ 604 AA; 62528 MW; 82B947C78366C071 CRC64;

Query Match 70.5%; Score 98; DB 1; Length 604;
 Best Local Similarity 68.0%; Pred. No. 5.5e-07; Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YQCELGKGSFSDKSNLTRHRIHTG 25
 Db 521 YRCSSCKKSISDSSRITKHLRIHSG 545

Search completed: January 6, 2004, 16:11:03
 Job time : 12 secs

C;Genetics: A;Note: D4RZP434J0650.1

A;Cross-references: EMBL:U35376; NID:91017721; PIDN:AAA79179.1; PID:91017722

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 01-Dec-2000

R;Accession: G02075

R;Poncet, D.A.

R;Submitted to the EMBL Data Library, September 1995

R;Reference number: G09169

R;Accession: G02075

R;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-595 <PON>

A;Cross-references: EMBL:U35376; NID:91017721; PIDN:AAA79179.1; PID:91017722

A;Gene: GBR:ZN985

A;Map position: 19p12-19p12

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 71.9%; Score 100; DB 2; Length 1191;

Best Local Similarity 68.0%; Pred. No. 6.8e-07; 4; Mismatches 5; Indels 0; Gaps 0;

Matches 17; Conservative 4; Gaps 0;

QY 1 YQCEIGGKSFSDKSNTLTHRLRIHTG 25

Db 192 YKCEBGGKAFRNSNLTRHKKIHTG 216

RESULT 3

S52411

ZNF165 protein - human

C;Species: Homo sapiens (man)

C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999

R;Tirozoutis, K.; Divane, A.; Jones, M.; Afara, N.

R;Submitted to the EMBL Data Library, February 1995

A;Description: Characterization of a novel zinc finger gene mapping to 6p21 which is exp

A;Accession: S52411

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-485 <TIR>

A;Cross-references: EMBL:X84801; NID:9683470; PIDN:CA459268.1; PID:9683471

Query Match 72.7%; Score 101; DB 2; Length 485;

Best Local Similarity 68.0%; Pred. No. 9.9e-07; 4; Mismatches 4; Indels 0; Gaps 0;

Matches 17; Conservative 4; Gaps 0;

QY 1 YQCEIGGKSFSDKSNTLTHRLRIHTG 25

Db 372 YECNEBGKSFASSESDLTRHRRHTG 396

RESULT 4

S47070

finger protein HZF9. Krueppel-related - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

R;Averkogn, M.; Hellman, L.

R;Submitted to the EMBL Data Library, June 1994

A;Description: Isolation of cDNA clones for 42 different Krueppel-related zinc finger pr

A;Reference number: S47065

A;Accession: S47070

A;Molecule type: mRNA

A;Residues: 1-247 <ABR>

R;Averkogn, M.; Averkogn, M.; Hellman, L.

DNA Cell Biol. 14, 125-136, 1995

A;Title: Isolation of cDNA clones for 42 different Krueppel-related zinc finger proteins

A;Reference number: I35566; MUID:9516221; PMID:786130

A;Accession: I35575

A;Molecule type: mRNA

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-247 <RES>

A;Cross-references: EMBL:X78932; NID:9498735; PIDN:CAA55532.1; PID:9498736

C;Genetics:

A;Gene: HZF9

C;Keywords: DNA binding; zinc finger

Query Match 71.9%; Score 100; DB 2; Length 1191;

Best Local Similarity 68.0%; Pred. No. 2.8e-06; 4; Mismatches 5; Indels 0; Gaps 0;

Matches 17; Conservative 3; Gaps 0;

QY 1 YQCEIGGKSFSDKSNTLTHRLRIHTG 25

Db 994 YKCEBGGKAFRNSNLTRHKKIHTG 1018

RESULT 7

I38599

zinc finger protein ZNF134 - human

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 05-Nov-1999

R;Tommerup, N.; Vibessing, H.

Genomics 27, 259-264, 1995

A;Title: Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identi

A;Reference number: A57785; MUID:9604430; PMID:7557990

A;Accession: I38599

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-348 <RES>

A;Cross-references: EMBL:U09412; NID:9488552; PIDN:AC50253.1; PID:9488553

RESULT 5

C;Genetics:
A;Gene: GDB:ZNF134
A;Cross-references: GDB:137033
A;Map position: 19q13.4-19q13.4

Query Match 71.2%; Score 99; DB 2; Length 348;
Best Local Similarity 68.0%; Pred. No. 1.3e-06; 3; Mismatches 5; Indels 0; Gaps 0;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YCCEICGSFSFSKSNLTRHLRHTG 25
Db 153 YECSECGKPKFSRKNLTRHLRHTG 177

RESULT 8

A39240 finger protein m91 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 05-Nov-1999

R;Passaniti, C.; Falsani, A.; Caruso, M.; Amati, P.
Proc. Natl. Acad. Sci. U.S.A. 86, 9417-9421, 1989
A;Title: Mouse genes coding for "zinc-finger"-containing proteins: characterization and
A;Reference number: A39240; MUID:90083278; PMID:2512575
A;Accession: A39240; MUID:90083278; PMID:2512575

A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: GB: M28513; NID:9199136; PIDN:AAA39531.1; PID:9554203
C;Keywords: DNA binding; zinc finger

Query Match 70.5%; Score 98; DB 2; Length 169;
Best Local Similarity 68.0%; Pred. No. 9.4e-07; 3; Mismatches 5; Indels 0; Gaps 0;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YCCEICGSFSFSKSNLTRHLRHTG 25
Db 92 YKCEECGKPKFSRKNLTRHLRHTG 116

RESULT 9

A56560 zinc finger protein/transactivator Zfp-38 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 01-Dec-2000

C;Accession: A56560; C48827
R;Choudhury, K.; Goulding, M.; Waltner, C.; Imai, K.; Fickenscher, H.
Mech. Dev. 39, 129-142, 1992
A;Title: The ubiquitous transactivator Zfp-38 is upregulated during spermatogenesis with
A;Reference number: A56560; MUID:93183757; PMID:1284028

A;Accession: A56560
A;Molecule type: mRNA
A;Residues: 1-150 <CHO>
A;Cross-references: GB:X63747; NID:955476; PIDN:CAA45280.1; PID:955477
A;Note: Experimental source: embryo
R;Noce, T.; Fujiwara, Y.; Sezaki, M.; Fujimoto, H.; Higashinakagawa, T.
Dev. Biol. 153, 35-36, 1992

A;Title: Expression of a mouse zinc finger protein gene in both spermatocytes and oocyte
A;Reference number: A48827; MUID:93012481; PMID:1397691
A;Accession: C48827
A;Molecule type: mRNA
A;Residues: 1-152, 'T', 194-494, 'E', 496-506, 'F', 508-509, 'S', 511-555 <NOC>
A;Cross-references: EMBL:D10620; NID:9220640; PIDN:BA001480.1; PID:9220641
A;Experimental source: spermatogenic cells; clone C48827
A;Note: sequence extracted from NCB1 backbone (NCBIP:114773)
C;Genetics:

A;Gene: Zfp-38
A;Map Position: 5
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: spermatogenesis; transcription regulation; zinc finger

Best Local Similarity 68.0%; Pred. No. 2.7e-06;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 YCCEICGSFSFSKSNLTRHLRHTG 25
Db 442 YCCEICGSFSFSKSNLTRHLRHTG 466

RESULT 10

S05447 finger protein glass - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000

C;Accession: S05447
A;Residues: 1-604 <MO>

R;Moses, K.; Ellis, M.C.; Rubin, G.M.
Nature 340, 531-536, 1989

A;Title: The glass gene encodes a zinc-finger protein required by Drosophila photorecep

A;Reference number: S05447; MUID:89365138; PMID:2770860

A;Molecule type: DNA

A;Cross-references: EMBL:X15400; NID:98015; PIDN:CA33450.1; PID:98016

A;Note: 60-Gln, 361-Ser, 362-Leu, and 377-Thr were also found

C;Genetics:

A;Gene: glass

A;Cross-references: FlyBase:FBgn004618

A;Map position: 3R 91112

A;Intron: 161; 59/3; 55/2

C;Keywords: DNA binding; nucleus; transcription factor; zinc finger

F:439-571/Region: zinc fingers

Query Match 70.5%; Score 98; DB 2; Length 604;
Best Local Similarity 68.0%; Pred. No. 2.9e-05; 3; Mismatches 5; Indels 0; Gaps 0;

Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YCCEICGSFSFSKSNLTRHLRHTG 25
Db 521 YRSSCKSKPSDSSTLTHRLHSG 545

RESULT 11

T46469 hypothetical protein DKFZ0434G1930.1 - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C;Accession: T46469
R;Blum, H.; Bauersch, S.; Meines, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000

A;Reference number: T46469
A;Accession: T46469
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-319 <AA>

A;Cross-references: EMBL:AI137483
A;Experimental source: adult testis; clone DKFZ0434G1930

A;Note: DKFZ0434G1930.1

Query Match 69.8%; Score 97; DB 2; Length 319;
Best Local Similarity 72.0%; Pred. No. 2.3e-06; 1; Mismatches 6; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YCCEICGSFSFSKSNLTRHLRHTG 25
Db 205 YKCEECGKPKFSRKNLTRHLRHTG 229

RESULT 12

D4284 finger protein ZNF50 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

C;Accession: D4284

Query Match 70.5%; Score 98; DB 2; Length 555;

R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.

Genomics 13, 999-1007, 1992

A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile si

A;Reference number: A43284; MUID:92372070; PMID:150591

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-88 <LIC>

A;Cross-references: GB:MA8360; NID:9340457; PID:9340458

A;Note: sequence extracted from NCBI backbone (NCBIN:111638, NCBIPI:111639)

C;Keywords: zinc finger

Query Match 69.1%; Score 96; DB 2; Length 88;
Best Local Similarity 60.0%; Pred. No. 1e-05; Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCCEBICKGSFSKSNTRHHLRHTG 25

Db 11 YCDCAGKAFPSQSTHQLHQRIHTG 35

RESULT 13

I38615 zinc finger protein ZNF19 - human (fragment)

N;Alternate names: finger protein kox18

C;Species: Homo sapiens (man)

C;Accession: 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 01-Dec-2000

C;Accession: I38616; I37957; S10406

R;Tommerup, N.; Viscontini, H.

Genomics 27, 259-264, 1995

A;Title: Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identif

A;Reference number: A57785; MUID:96044430; PMID:7557990

A;Molecule type: mRNA

A;Residues: 1-25 <RBS>

A;Cross-references: EMBL:U09848; NID:9495567; PIDN: AAC50264.1; PID:9495568

R;Milesen, H.J.; New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288309

A;Accession: I37957

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: EMBL:U09848; NID:9495567; PIDN: AAC50264.1; PID:9495568

R;Milesen, H.J.; New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288309

A;Accession: I37957

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: EMBL:U09848; NID:9495567; PIDN: AAC50264.1; PID:9495568

R;Milesen, H.J.; New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288309

A;Accession: I37957

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: EMBL:U09848; NID:9495567; PIDN: AAC50264.1; PID:9495568

R;Milesen, H.J.; New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288309

A;Accession: I37957

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: EMBL:U09848; NID:9495567; PIDN: AAC50264.1; PID:9495568

R;Milesen, H.J.; New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288309

A;Accession: I37957

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: EMBL:U09848; NID:9495567; PIDN: AAC50264.1; PID:9495568

R;Milesen, H.J.; New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288309

A;Accession: I37957

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-396 <WWM>

A;Cross-references: EMBL:AL080143

A;Experimental source: adult testis; clone DKFZp434N043

C;Genetics:

A;Note: DKFZp434N043-1

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 69.1%; Score 96; DB 2; Length 386;

Best Local Similarity 60.0%; Pred. No. 3.8e-06; Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCCEBICKGSFSKSNTRHHLRHTG 25

Db 301 YRCGECKAFAOKANLHQRIHTG 325

RESULT 15

S15917 developmental control protein mkrl - mouse

N;Alternate names: finger protein zfp-1

C;Species: Mus musculus (house mouse)

C;Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 01-Dec-2000

C;Accession: S15917; A26395; S06773

R;Chowdhury, K.; Dietrich, S.; Balling, R.; Guenet, J.L.; Gruss, P.

A;Title: Structure, expression and chromosomal localization of zfp-1, a murine zinc fi

A;Reference number: S15917; MUID:9098878; PMID:2574853

A;Accession: S15917

A;Molecule type: mRNA

A;Residues: 1-424 <CHO>

A;Cross-references: EMBL:X16493; NID:G55482; PIDN:CAA34510.1; PID:955483

R;Chowdhury, K.; Dietrich, U.; Gruss, P.

Cell 48, 771-778, 1987

A;Title: A multigene family encoding several "finger" structures is present and differ

A;Reference number: A90892; MUID:87131089; PMID:3815523

A;Accession: A26395

A;Molecule type: DNA

A;Residues: 'AEG' 1-424 <CHO2>

A;Cross-references: GB: M15708; NID:9193349; PIDN: AAA37639.1; PID:9387162

C;Genetics:

A;Gene: zfp-1

C;Keywords: zinc finger protein ZFP-36; LIM metal-binding repeat homology

C;Keywords: DNA binding; zinc finger

Query Match 69.1%; Score 96; DB 2; Length 424;

Best Local Similarity 60.0%; Pred. No. 4.2e-06; Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YCCEBICKGSFSKSNTRHHLRHTG 25

Db 197 YCDDVCKTFSHKANLHQRIHTG 221

RESULT 14

T12527 hypothetical protein DKFZp434N043.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 01-Dec-2000

C;Accession: T12527

R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, June 1999

A;Accession: T12527

A;Status: preliminary

A;Molecule type: mRNA

Search completed: January 6, 2004, 16:13:00

Job time: 23 secs

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

Om protein - protein search, using sw model

Run on: January 6, 2004, 16:11:57 ; search time 33 Seconds

(without alignments) 152.001 Million cell updates/sec

Title: US-09-774-940A-1

Perfect score: 139

Sequence: 1 YQCICIGKSFSKSNLTHRLIRHTG 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters:

733937

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pbpa/US07_PUBCOMB_pep:*

2: /cgn2_6/ptodata/1/pbpa/US07_PUBCOMB_pep:*

3: /cgn2_6/ptodata/1/pbpa/US06_PUBCOMB_pep:*

4: /cgn2_6/ptodata/1/pbpa/US05_PUBCOMB_pep:*

5: /cgn2_6/ptodata/1/pbpa/US04_PUBCOMB_pep:*

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9: /cgn2_6/ptodata/1/pbpa/US08_PUBCOMB_pep:*

10: /cgn2_6/ptodata/1/pbpa/US09_PUBCOMB_pep:*

11: /cgn2_6/ptodata/1/pbpa/US09C_PUBCOMB_pep:*

12: /cgn2_6/ptodata/1/pbpa/US09_NNEW_PUB_pep:*

13: /cgn2_6/ptodata/1/pbpa/US10A_PUBCOMB_pep:*

14: /cgn2_6/ptodata/1/pbpa/US10B_PUBCOMB_pep:*

15: /cgn2_6/ptodata/1/pbpa/ZINC_PUBCOMB_pep:*

16: /cgn2_6/ptodata/1/pbpa/US10_NNEW_PUB_pep:*

17: /cgn2_6/ptodata/1/pbpa/US60_PUBCOMB_pep:*

18: /cgn2_6/ptodata/1/pbpa/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	139	100.0	25	10	US-09-774-940A-1
2	108	77.7	29	9	Sequence 1, Appli
3	108	77.7	29	11	Sequence 9, Appli
4	108	77.7	29	11	Sequence 9, Appli
5	108	77.7	29	12	Sequence 9, Appli
6	106	76.3	561	12	Sequence 9, Appli
7	104	74.8	362	15	Sequence 9, Appli
8	104	74.8	525	9	Sequence 9, Appli
9	104	74.8	576	12	Sequence 9, Appli
10	103	74.1	409	12	Sequence 9, Appli
11	103	74.1	475	12	Sequence 9, Appli
12	102	73.4	25	15	Sequence 9, Appli
13	102	73.4	530	12	Sequence 9, Appli
14	100	71.9	242	12	Sequence 9, Appli
15	100	71.9	295	12	Sequence 9, Appli

FEATURES

; OTHER INFORMATION: CYS-CYS-HIS-HIS ZINC FINGER

US-09-774-940A-1

Query Match Similarity 100.0%; Score 139; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. 5.9e-13; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQCICIGKSFSKSNLTHRLIRHTG 25

Ds 1 YQCICIGKSFSKSNLTHRLIRHTG 25

RESULT 2
US-09-851-271A-9
; Sequence 9, Application US/09851271A
; Patent No. US2002004824A1
; GENERAL INFORMATION:

APPLICANT: Gendaq Limited
 TITLE OF INVENTION: Screening System
 FILE REFERENCE: 67438-2003
 CURRENT APPLICATION NUMBER: US/09/851,271A
 PRIORITY FILING DATE: 2001-05-08
 PRIORITY APPLICATION NUMBER: PCT/GB99/03730
 PRIORITY FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 156
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 9
 LENGTH: 29
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: ZN FING
 LOCATION: (1)..(29)
 OTHER INFORMATION: zinc finger consensus structure
 US-09-851-271A-9

RESULT 3
 Query Match Best Local Similarity 77.7%; Score 108; DB 9; Length 29;
 Best Local Similarity 76.0%; Pred. No. 1-7e-08; Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YQCEICKGKPSDKNLTRHLRILHG 25
 Db 2 YKCSBCKGKAFSQKSNLTRHQRIHG 26

US-09-995-973-9
 Sequence 9, Application US/09995973
 Publication No. US20030024006A1
 GENERAL INFORMATION:
 APPLICANT: CHOO, Yen
 APPLICANT: ULLMAN, Christopher G.
 TITLE OF INVENTION: GENE SWITCHES
 FILE REFERENCE: 8328-2003 / GT-US1
 CURRENT APPLICATION NUMBER: US/09/995,973
 CURRENT FILING DATE: 2002-03-19
 NUMBER OF SEQ ID NOS: 59
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 9
 LENGTH: 29
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: consensus
 US-09-995-973-9

RESULT 4
 US-09-995-984-9
 Sequence 9, Application US/099956484
 Publication No. US20030092010A1
 GENERAL INFORMATION:
 APPLICANT: CHOO, Yen
 APPLICANT: ULLMAN, Christopher G.
 TITLE OF INVENTION: MOLECULAR SWITCHES
 FILE REFERENCE: 8328-2004 / GT-US1
 CURRENT APPLICATION NUMBER: US/09/996,484
 CURRENT FILING DATE: 2002-04-08
 NUMBER OF SEQ ID NOS: 64

RESULT 5
 US-10-192-078-23
 Sequence 23, Application US/10192078
 Publication No. US20030189331A1
 GENERAL INFORMATION:
 APPLICANT: CHOO, Yen
 APPLICANT: Ullman, Christopher Graeme
 APPLICANT: Chua, Nam-Hai
 APPLICANT: Sanchez, Juan Pablo
 TITLE OF INVENTION: Regulated Gene Expression in Plants
 FILE REFERENCE: 674538-2001.3
 CURRENT APPLICATION NUMBER: US/10/192,078
 CURRENT FILING DATE: 2002-11-03
 PRIORITY FILING DATE: 2000-12-07
 PRIORITY APPLICATION NUMBER: PCT/GB00/02071
 PRIORITY FILING DATE: 2000-05-30
 PRIORITY APPLICATION NUMBER: UK 001580.0
 PRIORITY FILING DATE: 2000-12-07
 PRIORITY APPLICATION NUMBER: 09/732,348
 PRIORITY FILING DATE: 2000-01-24
 PRIORITY APPLICATION NUMBER: UK 9912635.1
 PRIORITY FILING DATE: 1999-05-18
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 23
 LENGTH: 29
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Consensus zinc finger structure
 US-10-192-078-23

RESULT 6
 US-10-104-047-2805
 Sequence 2805, Application US/10104047
 Publication No. US20030236392A1
 GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: No. US20030236392A1 full length cDNA
 FILE REFERENCE: H1-A0105
 CURRENT APPLICATION NUMBER: US/10/104,047
 CURRENT FILING DATE: 2002-03-25
 PRIORITY APPLICATION NUMBER:
 PRIORITY FILING DATE:

NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2805
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2805

Query Match 76.3%; Score 106; DB 12; Length 561;
Best Local Similarity 76.0%; Pred. No. 7.8e-07; Mismatches 4; Indels 0; Gaps 0;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YOCEICKSFSDKSNLTRHLRHTG 25
Db 411 YECNECKSFSPKSTLKHRLRHTG 435

RESULT 7
US-10-043-487-390
; Sequence 390, Application US/10043487
; Sequence No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: PIERRE LIEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptides
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: BA77BA
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIORITY APPLICATION NUMBER: US 60/261,130
; PRIORITY FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 390
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Shigella Flexneri
; US-10-043-487-390

Query Match 74.8%; Score 104; DB 15; Length 362;
Best Local Similarity 76.0%; Pred. No. 9.4e-07; Mismatches 5; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YOCEICKSFSDKSNLTRHLRHTG 25
Db 108 YOCECKSFSQCLCNLTRHLRHTG 132

RESULT 8
US-09-864-761-33653
; Sequence 33653, Application US/09864761
; PRIORITY NUMBER: US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIORITY APPLICATION NUMBER: US 60/180,312
; PRIORITY FILING DATE: 2000-02-04 456
; PRIORITY APPLICATION NUMBER: US 60/207,456
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: US 09/632,366
; PRIORITY FILING DATE: 2000-08-03
; PRIORITY APPLICATION NUMBER: GB 24263,6
; PRIORITY FILING DATE: 2000-10-04
; PRIORITY APPLICATION NUMBER: US 60/236,359
; PRIORITY FILING DATE: 2000-09-27
; PRIORITY APPLICATION NUMBER: PCT/US01/00666

RESULT 9
US-10-034-749-2365
; Sequence 2365, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSU, TENSUI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUKO
; APPLICANT: HIO, YURI
; APPLICANT: OOSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKI, ICHIRO ; SOFTWARE: PatentIn Ver. 2.1
 APPLICANT: SERKI NAOKI ; SEQ ID NO: 3470
 APPLICANT: YOSHIKAWA, TSUTOMU ; LENGTH: 475
 APPLICANT: OTSUKA, MOTYUKI ; TYPE: PRT
 APPLICANT: NAGAHATA, KENJI ; ORGANISM: Homo sapiens
 APPLICANT: MASUHO, YASHIKO ; -10-047-3470
 TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
 FILE REFERENCE: 084335/0160
 CURRENT APPLICATION NUMBER: US/10/094,749
 CURRENT FILING DATE: 2002-03-12
 PRIORITY APPLICATION NUMBER: 60/3350,435
 PRIORITY FILING DATE: 2002-01-24
 PRIORITY APPLICATION NUMBER: J 2001-328381
 PRIORITY FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 3381
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2365
 LENGTH: 576
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-094-749-2365

Query Match? 74.8%; Score 104; DB 12; Length 576;
 Best Local Similarity 72.0%; Pred. No. 1.5e-06; 3; Mismatches 4; Indels 0; Gaps 0;
 Matches 18; Conservative 3; QY 1 YCCEICGKSFSDKSNLIRIHTG 25
 1 YCCEICGKSFSDKSNLIRIHTG 25
 1 YCCEICGKSFSDKSNLIRIHTG 517
 Db 493 YCNECGKAFNQSHLIRIHTG 446

RESULT 10 US-10-104-047-2663
 ; Sequence 78, Application US/10198677
 ; Publication No. US20030119023A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOO, Yen
 ; APPLICANT: KLUG, Aaron
 ; APPLICANT: MOORE, Michael
 ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: NUCLEAR ACID BINDING POLYPEPTIDES CHARACTERIZED BY
 ; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
 ; FILE REFERENCE: 8325-2011 / G1-US1
 ; CURRENT APPLICATION NUMBER: US/10/198,677
 ; CURRENT FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 144
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 78
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequence: consensus structure
 US-10-198-677-78

Query Match? 74.1%; Score 103; DB 12; Length 409;
 Best Local Similarity 72.0%; Pred. No. 1.5e-06; 3; Mismatches 4; Indels 0; Gaps 0;
 Matches 18; Conservative 3; QY 1 YCCEICGKSFSDKSNLIRIHTG 25
 1 YCCEICGKSFSDKSNLIRIHTG 25
 1 YCCEICGKSFSDKSNLIRIHTG 381
 Db 357 YCNECGKAFNQSHLIRIHTG 381

RESULT 11 US-10-104-047-3470
 ; Sequence 3470, Application US/10104047
 ; Publication No. US20030236392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
 ; FILE REFERENCE: HI-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIORITY APPLICATION NUMBER:
 ; PRIORITY FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 3434
 ; LENGTH: 530
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-104-047-3434

Query Match? 73.4%; Score 102; DB 12; Length 530;
 Best Local Similarity 68.0%; Pred. No. 2.7e-06; 5; Mismatches 5; Indels 0; Gaps 0;
 Matches 17; Conservative 3; QY 1 YCCEICGKSFSDKSNLIRIHTG 25
 1 YCCEICGKSFSDKSNLIRIHTG 25
 1 YCCEICGKSFSDKSNLIRIHTG 446
 Db 422 YCNECGKAFNQSHLIRIHTG 446

RESULT 12 US-10-198-677-78
 ; Sequence 78, Application US/10198677
 ; Publication No. US20030119023A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOO, Yen
 ; APPLICANT: KLUG, Aaron
 ; APPLICANT: MOORE, Michael
 ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: NUCLEAR ACID BINDING POLYPEPTIDES CHARACTERIZED BY
 ; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
 ; FILE REFERENCE: 8325-2011 / G1-US1
 ; CURRENT APPLICATION NUMBER: US/10/198,677
 ; CURRENT FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 144
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 78
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequence: consensus structure
 US-10-198-677-78

Query Match? 73.4%; Score 102; DB 15; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.1e-07; 2; Mismatches 4; Indels 0; Gaps 0;
 Matches 18; Conservative 2; QY 1 YCCEICGKSFSDKSNLIRIHT 24
 1 YCCEICGKSFSDKSNLIRIHT 24
 2 YCNECGKAFNQSHLIRIHT 25
 Db 2 YCNECGKAFNQSHLIRIHT 25

Qy 1 YQCETCGKSPSDKSNLTHRLRHTG 25 ; PRIORITY FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3181
 ; Db 438 YACTIVCGKAFSQSNLTHHEKHTG 462 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1859 ;
 ; LENGTH: 295 ;
 ;
 RESULT 14 ;
 ; Sequence 33120, Application US/10029386 ;
 ; Publication No. US20030194704A1 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G ;
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO ;
 ; FILE REFERENCE: AEONICX-X-2 ;
 ; CURRENT APPLICATION NUMBER: US/10/029,386 ;
 ; CURRENT FILING DATE: 2001-12-20 ;
 ; NUMBER OF SEQ ID NOS: 34288 ;
 ; SOFTWARE: Annotax Sequence Listing Engine vers. 1.1 ;
 ; SEQ ID NO 33120 ;
 ; LENGTH: 242 ;
 ;
 ; TYPE: PRT ;
 ; ORGANISM: Homo sapiens ;
 ;
 FEATURE: ;
 ; OTHER INFORMATION: MAP TO AF205588.1 ;
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1 ;
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3 ;
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2 ;
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.89 ;
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3 ;
 ; OTHER INFORMATION: SWISSPROT HIT: Q06730, EVALUE 2.00e-84 ;
 ; US-10-029-386-33120 ;
 ;
 Query Match 71.9%; Score 100; DB 12; Length 242;
 Best Local Similarity 70.8%; Pred. No. 2.3e-06;
 Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YQCETCGKSPSDKSNLTHRLRHTG 24 ;
 ; Db 219 YCNECGKAFSQSNLTHHEKHTG 242 ;
 ;
 RESULT 15 ;
 US-10-094-749-1859 ;
 ; Sequence 1859, Application US/10094749 ;
 ; Publication No. US2003019741A1 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: ISOGAI, TAKAO ;
 ; APPLICANT: SUGIYAMA, TOMOYASU ;
 ; APPLICANT: OTSUKI, TETSUJI ;
 ; APPLICANT: WAKAMATSU, AI ;
 ; APPLICANT: SATO, HIROYUKI ;
 ; APPLICANT: ISHII, SHIZUKO ;
 ; APPLICANT: YAMAMOTO, JUN-ICHI ;
 ; APPLICANT: ISONO, YUKO ;
 ; APPLICANT: HIO, YURI ;
 ; APPLICANT: OTSUKA, KAORU ;
 ; APPLICANT: NAGAI, KEIICHI ;
 ; APPLICANT: IRIE, RYOTARO ;
 ; APPLICANT: TAMEICHIKA, ICHIRO ;
 ; APPLICANT: SEKI, NAOHIKO ;
 ; APPLICANT: YOSHIKAWA, TSUTOMU ;
 ; APPLICANT: OTSUKA, MOTOKI ;
 ; APPLICANT: NAGAHARI, KENJI ;
 ; APPLICANT: MASUHO, YASUHIKO ;
 ;
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA ;
 ; FILE REFERENCE: 094335/0160 ;
 ; CURRENT APPLICATION NUMBER: US/10/094,749 ;
 ; CURRENT FILING DATE: 2002-03-12 ;
 ; PRIORITY APPLICATION NUMBER: 6/03350,435 ;
 ; PRIORITY FILING DATE: 2002-01-24 ;
 ; PRIORITY APPLICATION NUMBER: JP 2001-328381 ;
 ;
 ; Search completed: January 6, 2004, 16:17:24 ;
 ; Job time : 34 sec ;

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OM protein - protein search, using sw model.

Run on: January 6, 2004, 16:09:06 ; Search time 22 Seconds

(without alignments) 48.081 Million cell updates/sec

Title: US 09-774-940A-1

Perfect score: 139

Sequence: 1 YQCETCGKSSSDKSNLTHRLRHTG 25

Scoring table: BIOSUMK2

Gapop 11.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5a_COMBO_pep:*

2: /cgn2_6/ptodata/1/iaa/5b_COMBO_pep:*

3: /cgn2_6/ptodata/1/iaa/6a_COMBO_pep:*

4: /cgn2_6/ptodata/1/iaa/6b_COMBO_pep:*

5: /cgn2_6/ptodata/1/iaa/PCITS_COMBO_pep:*

6: /cgn2_6/ptodata/1/iaa/bactfile1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	102	73.4	89	3 US-09-774-940B-18
2	102	73.4	89	3 US-09-774-940B-18
3	96	69.1	26	2 US-08-620-151-84
4	94	67.6	671	3 US-09-121-321-16
5	94	67.6	671	3 US-08-620-151-84
6	65.9	151	4	US-09-333-803A-16
7	65.9	151	4	US-09-389-956-64
8	92	66.2	26	2 US-08-91-537A-15
9	92	66.2	26	2 US-08-91-537A-15
10	92	66.2	26	2 US-08-620-151-84
11	92	66.2	26	2 US-08-620-151-84
12	92	66.2	41	2 US-09-389-831-15
13	92	66.2	488	2 US-08-933-750C-17
14	92	66.2	488	3 US-09-234-613-17
15	91	65.5	56	4 US-08-733-622C-33
16	91	65.5	208	4 US-08-733-622C-37
17	91	65.5	209	4 US-08-733-622C-8
18	91	65.5	507	4 US-08-733-622C-2
19	91	65.5	640	3 US-09-262-773-4
20	91	65.5	648	3 US-09-362-773-2
21	90	64.7	26	2 US-08-220-151-78
22	89	64.0	25	2 US-08-220-151-98
23	89	64.0	543	4 US-09-362-123A-4
24	88	63.3	26	2 US-08-220-151-30
25	88	63.3	26	2 US-08-620-151-37
26	88	63.3	711	3 US-09-220-170A-10
27	88	63.3	711	3 US-09-055-659-10

ALIGNMENTS

RESULT 1

US-09-774-940B-18

; Sequence 18, Application US/08793408
 ; Patent No. 600788
 ; GENERAL INFORMATION:

; APPLICANT: Cho, Yen
 ; APPLICANT: KIUG, Aaron
 ; APPLICANT: Sanchez Garcia, Isidro

; TITLE OF INVENTION: Improvements in or Relating to
 ; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:
 ; SOFTWARE: Word Perfect
 ; APPLICATION NUMBER: US/08/793,408

; FILING DATE:
 ; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/01949

; FILING DATE: 17-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9514698.1
 ; FILING DATE: 18-JUL-1995

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9422534.9

; FILING DATE: 08-NOV-1994

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9416880.4

; FILING DATE: 20-AUG-1994

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 89 amino acids

; TYPE: amino acid
 ; STRANDEDNESS: 2

; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein

; Best Local Similarity 73.4%; Score 102; DB 3; Length 89;
 ; Query Match 73.4%; Score 102; DB 3; Length 89;
 ; Best Local Similarity 68.0%; Pred. No. 7.3e-08;

Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Query 1 YQCETQGKSSDKSNLTHRIKHTG 25 ; Sequence 18; Application US/09139762A ; Patent No. 6013453

Db 63 FQCRICMRNFSDRSLNTRHRTHG 87

RESULT 2 US-09-139-762A-18

GENERAL INFORMATION:

APPLICANT: Choo, Yen

APPLICANT: Klug, Aaron

APPLICANT: Sanchez Garcia, Isidro

TITLE OF INVENTION: Improvements in or Relating to TITLE OF INVENTION: Binding Proteins for Recognition of DNA NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury, Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/139, 762A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/793, 408

FILING DATE: 02-JUN-1997

APPLICATION NUMBER: PCT/GB95/01949

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9514698.1

FILING DATE: 18-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 94122534.9

FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9416880.4

FILING DATE: 20-AUG-1994

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 89 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: Protein

US-09-139-762A-18

RESULT 3 US-08-620-151-84

Query Match 73.4%; Score 102; DB 3; Length 89; Best Local Similarity 68.0%; Pred. No. 7.3e-08; Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Gaps 0; Query 1 YQCETQGKSSDKSNLTHRIKHTG 25 ; Sequence 17; Application US/08620151 ; Patent No. 5928955

GENERAL INFORMATION:

APPLICANT: Imperiali, Barbara

APPLICANT: Walkup, Grant K.

RESULT 3 US-08-620-151-84

Query Match 73.4%; Score 102; DB 3; Length 89; Best Local Similarity 68.0%; Pred. No. 7.3e-08; Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Gaps 0; Query 1 YQCETQGKSSDKSNLTHRIKHTG 25 ; Sequence 17; Application US/08620151 ; Patent No. 5928955

GENERAL INFORMATION:

APPLICANT: Imperiali, Barbara

APPLICANT: Walkup, Grant K.

RESULT 4 US-09-121-321-16

Query Match 69.1%; Score 96; DB 2; Length 26; Best Local Similarity 60.0%; Pred. No. 1.5e-07; Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0; Gaps 0; Query 1 YQCETQGKSSDKSNLTHRIKHTG 25 ; Sequence 16; Application US/09121321 ; Patent No. 6090783

GENERAL INFORMATION:

APPLICANT: Saiga, Akihiko

APPLICANT: Orita, Satoru

APPLICANT: Igarashi, Hisanaga

APPLICANT: Okumura, Koushi

APPLICANT: Sabaguchi, Gaku

TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/121, 321

FILING DATE:

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,151

FILED DATE: 22-MAR-1996

CLASSIFICATION: 422

ATTORNEY/AGENT INFORMATION:

NAME: Shannon, Karen L.

REGISTRATION NUMBER: 36,675

REFERENCE/DOCKET NUMBER: 8597/6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-321-4200

TELEFAX: 312-321-4299

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-620-151-57

Query Match 66.2%; Score 92; DB 2; Length 26;
Best Local Similarity 64.0%; Pred. No. 5.6e-07;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YOCEBICGKSKSDKSNTLTHRLRIHTG 25

Db 2 YTCBEGGKSFQSQSSALVKAIVRIHTG 26

RESULT 10

US-08-620-151-58

Sequence 58. Application US/08620151

Patent No. 592895

GENERAL INFORMATION:

APPLICANT: Imperilli, Barbara

APPLICANT: Walkup, Grant K.

TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR

TITLE OF INVENTION: DIVALENT ZINC

NUMBER OF SEQUENCES: 136

CORRESPONDENCE ADDRESS:

ADDRESSEE: BRINKS, HOFFER, GILSON & LIONE

STREET: NBC Tower - Suite 3600, 455 N. Cityfront

CITY: Chicago

STATE: Illinois

ZIP: 60611-5599

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,151

FILED DATE: 22-MAR-1996

CLASSIFICATION: 422

ATTORNEY/AGENT INFORMATION:

NAME: Shannon, Karen L.

REGISTRATION NUMBER: 36,675

REFERENCE/DOCKET NUMBER: 8597/6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-321-4200

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: linear

MOLECULE TYPE: peptide

US-08-491-527A-15

Query Match 66.2%; Score 92; DB 2; Length 26;

Best Local Similarity 64.0%; Pred. No. 5.6e-07;

Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YOCEBICGKSKSDKSNTLTHRLRIHTG 25

Db 2 YTCBEGGKSFQSQSSALVKAIVRIHTG 26

RESULT 9

US-08-620-151-57

Sequence 57. Application US/08620151

Patent No. 592895

GENERAL INFORMATION:

APPLICANT: Imperilli, Barbara

APPLICANT: Walkup, Grant K.

TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR

TITLE OF INVENTION: DIVALENT ZINC

NUMBER OF SEQUENCES: 136

CORRESPONDENCE ADDRESS:

ADDRESSEE: BRINKS, HOFER, GILSON & LIONE

STREET: NBC Tower - Suite 3600, 455 N. Cityfront

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60611-5599

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: peptide

Query Match: Similarity 66.2%; Score 92; DB 2; Length 26;
 Best Local Similarity 64.0%; Pred. No. 5.6e-07; Mismatches 7; Indels 0; Gaps 0;
 Matches 16; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 YCCEICKSFSKSNTRHRIHTG 25
 Db 2 YACSTCGKSFQKSDLAKHQRIHTG 26

RESULT 11
 US-09-620-151-89
 Sequence 89, Application US/08620151
 Patent No. 5928955
 GENERAL INFORMATION:
 APPLICANT: Walkup, Grant K.
 TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
 TITLE OF INVENTION: DIVALENT ZINC
 NUMBER OF SEQUENCES: 136
 CORRESPONDENCE ADDRESS:
 ADDRESSE: BRINKS, HOFER, GILSON & LIONE
 STREET: NBC Tower - Suite 3600, 455 N. Cityfront
 STREET: Plaza Drive
 STATE: Illinois
 CITY: Chicago
 STATE: USA
 ZIP: 60611-5599
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,151
 FILING DATE: 22-MAR-1996
 CLASSIFICATION: 422
 ATTORNEY/AGENT INFORMATION:
 NAME: Shannon, Karen L.
 REGISTRATION NUMBER: 36,675
 REFERENCE/DOCKET NUMBER: 8597/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-21-4200
 TELEFAX: 312-321-4299
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-620-151-89

Query Match: Similarity 66.2%; Score 92; DB 2; Length 26;
 Best Local Similarity 64.0%; Pred. No. 5.6e-07; Mismatches 7; Indels 0; Gaps 0;
 Matches 16; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 YCCEICKSFSKSNTRHRIHTG 25
 Db 2 YCTECGKTSQRSTLHLHQRIHTG 26

RESULT 12
 US-09-389-831-15
 Sequence 15, Application US/09389831
 Patent No. 6621420
 GENERAL INFORMATION:
 APPLICANT: Herman, Ira M.
 APPLICANT: Siczekiewicz, Greg J.
 TITLE OF INVENTION: HYPERTENSION ASSOCIATED TRANSCRIPTION FACTORS AND USES THEREFOR
 FILE REFERENCE: MBI-006
 CURRENT APPLICATION NUMBER: US/09/389,831
 CURRENT FILING DATE: 1999-09-03
 NUMBER OF SEQ ID NOS: 19

Query Match: Similarity 66.2%; Score 92; DB 2; Length 488;
 Best Local Similarity 60.0%; Pred. No. 9.2e-07; Mismatches 6; Indels 0; Gaps 0;
 Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 YCCEICKSFSKSNTRHRIHTG 25
 Db 4 YCSCLOCKAFORSSVLUQHQRIHTG 28

RESULT 13
 US-08-933-750C-17
 Sequence 17, Application US/08933750C
 Patent No. 5932442
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Baranani, Olga
 APPLICANT: Shah, Purvi
 APPLICANT: Au-Young, Janice
 APPLICANT: Yue, Henry
 APPLICANT: Guseeler, Karl J.
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
 NUMBER OF SEQUENCES: 98
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/933,750C
 FILING DATE: September 23, 1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0356 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-825-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 488 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BR3NOT03
 CLONE: 641127
 US-08-933-750C-17